

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:07:22 ; Search time 95 Seconds

(without alignments)
43.461 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYCKEPMISAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	63.0	790	Q96MR9	Q96mr9 homo sapien
2	52	56.5	127	Q9DD23	Q9dd23 mus musculus
3	52	56.5	2841	Q8MLU9	Q8mlu9 drosophila
4	52	56.5	2931	Q9W2C6	Q9w2c6 drosophila
5	50	54.3	955	Q96DN2	Q96dn2 homo sapien
6	48.5	52.7	268	Q8MQH9	Q8mqh9 paracentrot
7	48	52.2	191	Q8BLCT	Q8blct mus musculus
8	48	52.2	240	Q9JLK8	Q9jlk8 mus musculus
9	48	52.2	243	Q9H163	Q9h163 homo sapien
10	48	52.2	243	Q9D0V2	Q9d0v2 mus musculus
11	48	52.2	243	Q8BLR4	Q8blr4 mus musculus
12	48	52.2	462	Q8L7I2	Q8l7i2 mus musculus
13	48	52.2	773	Q9H164	Q9h164 homo sapien
14	48	52.2	773	Q9QYE3	Q9qye3 mus musculus
15	48	52.2	776	Q9JIT4	Q9jit4 mus musculus
16	48	52.2	797	Q9H3G9	Q9h3g9 homo sapien

17	48	52.2	800	4	Q96JL6	Q96jl6 homo sapien
18	48	52.2	835	4	Q9H165	Q9h165 homo sapien
19	48	52.2	889	10	Q9FHH9	Q9fhh9 arabidopsis
20	47	51.1	129	11	Q920G7	Q920g7 mus musculus
21	47	51.1	367	2	Q9AJ67	Q9aj67 desulfovibr
22	47	51.1	472	16	Q9KFS9	Q9kfs9 chlorobium
23	46	50.0	225	17	Q29808	Q29808 archaeoglob
24	45	48.9	157	17	Q29312	Q29312 archaeoglob
25	45	48.9	443	11	Q8BLX6	Q8blx6 mus musculus
26	45	48.9	484	10	Q9FEL7	Q9fel7 medicago tr
27	45	48.9	1209	12	Q8JL60	Q8jlm60 manestria co
28	44	47.8	100	17	Q97BHS	Q97bhs thermoplasma
29	44	47.8	134	11	Q83318	Q83318 rattus norv
30	44	47.8	148	12	Q56946	Q56946 human papil
31	44	47.8	366	10	Q8S6L7	Q8s6l7 oryza sativ
32	44	47.8	388	5	Q17002	Q17002 anopheles g
33	44	47.8	391	16	Q9KCP4	Q9kcp4 bacillus ha
34	44	47.8	565	5	Q04134	Q04134 drosophila
35	43	46.7	61	4	Q8TE66	Q8te66 homo sapien
36	43	46.7	70	11	Q54837	Q54837 mus musculus
37	43	46.7	114	16	Q8YFW3	Q8ypw3 anabaena sp
38	43	46.7	148	5	Q9VLF3	Q9vlf3 drosophila
39	43	46.7	150	5	Q8MT42	Q8mt42 drosophila
40	43	46.7	204	5	Q81IA3	Q81ia3 drosophila
41	43	46.7	267	16	Q8RFU1	Q8rfu1 fusobacteri
42	43	46.7	295	5	Q8MQB4	Q8mqb4 caenorhabdi
43	43	46.7	295	16	Q8FFA1	Q8ffa1 escherichia
44	43	46.7	413	16	Q8XHM2	Q8xhm2 clostridium
45	43	46.7	449	10	Q8W047	Q8w047 oryza sativ

ALIGNMENTS

RESULT 1

Q96MR9 PRELIMINARY; PRT; 790 AA.
ID Q96MR9
AC Q96MR9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ31986.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kanihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK056548; BAB71213.1; --
DR InterPro: IPR001509; KRAB.
DR InterPro: IPR006895; zf-Sec23_Sec24.
DR InterPro: IPR007087; Znf C2H2.
DR Pfam: PF01352; KRAB; 2.
DR Pfam: PF00096; zf-C2H2; 14.
DR Pfam: PF04810; zf-Sec23_Sec24; 1.
DR SMART: SM00349; KRAB; 2.
DR SMART: SM00355; Znf C2H2; 14.
DR PROSITE: PS00805; KRAB; 2.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 13.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 14.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 790 AA; 91134 MW; BID7B3CC07C1179F CRC64;

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Query Match          63.0%; Score 58; DB 4; Length 790;
Best Local Similarity 64.3%; Pred. No. 0.14;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KCVYCKEPTWSAC 16
DB 517 KCVYCKGKPTSSAC 530

RESULT 2
Q9DD23 PRELIMINARY; PRT; 127 AA.
AC Q9DD23
AT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 0610005K03Rik protein.
GN 0610005K03Rik
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK002226; BAB21948.1; --
DR HSSP; PI3987; 1ERG.
DR MGD; MGI:1915561; 0610005K03Rik.
DR InterPro; IPR003632; LY-6_CD59.
DR Jfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 127 AA; 13279 MW; 9CCE20688671982C CRC64;

Query Match          56.5%; Score 52; DB 11; Length 127;
Best Local Similarity 46.7%; Pred. No. 0.31;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 LKCVYCKEPTWSAC 16
DB 23 LQCVYTCANPVSASNC 37

RESULT 3
Q8MLU9 PRELIMINARY; PRT; 2841 AA.
AC Q8MLU9
AT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE CG13492-PB.

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GN OS OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227; [1] SEQUENCE FROM N.A. STRAIN=Berkely; MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yeung M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Rogers J., Helt G., Nelson C.R., Milos B.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Fries B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Flosser K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C., Hoskins D., Houston K.A., Howland T.J., Wei M.-H., Ibegwack J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasmann D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000).

[2] SEQUENCE FROM N.A. Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Barzon J., An H., Baldwin D., Benson K.Y., Beeson K.Y., Busam D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J., Ibegwack M., Houch J., Hoskins R.A., Hostin D., Howland T.J., Mcintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragans V., Park S., Patel S., Pfeiffer B., Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of *Drosophila melanogaster* genome." Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3] SEQUENCE FROM N.A. Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tuzy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp N., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

CG13492. *Drosophila melanogaster* (Fruit fly). Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227; [1] SEQUENCE FROM N.A. STRAIN=Berkely; MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yeung M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Rogers J., Helt G., Nelson C.R., Milos B.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Fries B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Flosser K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C., Hoskins D., Houston K.A., Howland T.J., Wei M.-H., Ibegwack J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasmann D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of *Drosophila melanogaster*." Science 287:2185-2195 (2000).

```

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003455; AAM71018.1; -.
DR FlyBase; FBgn0034662; CG13492.
DR InterPro; IPR000173; CAP_dhdrogenase.
DR PROSITE; PS00071; GAPDH; 1.
SQ SEQUENCE 2841 AA; 306647 MW; 21E2A1B14455D494 CRC64;

Query Match 56.5%; Score 52; DB 5; Length 2841;
Best Local Similarity 47.4%; Pred. No. 4;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 LKCYCKEPM-----TSAAC 16
|:|||||:|:|
Db 1321 LECYCKDPFCEDPTTSC 1339

RESULT 4
Q9W2C6 PRELIMINARY; PRT; 2931 AA.
ID Q9W2C6
AC Q9W2C6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG13492 protein.
GN CG13492.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitsky A.A., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003455; AAF46766.2; -.
DR FlyBase; FBgn0034662; CG13492.
DR InterPro; IPR000173; CAP_dhdrogenase.
DR PROSITE; PS00071; GAPDH; 1.
SQ SEQUENCE 2931 AA; 316518 MW; B06C15D9DF257EF6 CRC64;

Query Match 56.5%; Score 52; DB 5; Length 2931;
Best Local Similarity 47.4%; Pred. No. 4.1;
Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 LKCYCKEPM-----TSAAC 16
|:|||||:|:|
Db 1411 LECYCKDPFCEDPTTSC 1429

RESULT 5
Q96DN2 PRELIMINARY; PRT; 955 AA.
ID Q96DN2
AC Q96DN2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32009.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Makamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuho K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056571; BAB71219.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001007; WVF_C.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00093; WVF; 5.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00214; VWC; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WVF_C; 5.
KW Hypothetical protein; EGF-like domain.
SQ SEQUENCE 955 AA; 99884 MW; 88B0DCABA8A9188 CRC64;

Query Match 54.3%; Score 50; DB 4; Length 955;
Best Local Similarity 53.8%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPM-----TSAAC 16
|:|||||:|:|

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ID Q9D0V2 PRELIMINARY; PRT; 243 AA.
AC Q9D0V2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 18 days embryo cDNA, RIKEN full-length enriched library,
clone.1110067K14, full insert sequence.
GN BCL11A OR EV19.
GE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Saaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL ENBL: AK004395; BAB23285.1; --
DR MGD; MGI:106190; Bcl11a.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF000096; zf-C2H2; 1.
DR SMART; SM00355; Znf_C2H2; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 243 AA; 26823 MW; B18CC391B83BC479 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 243;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CYTCKEPM TSA 14
Db 172 CTTCKQPFTA 182

RESULT 11
Q9BLR4 PRELIMINARY; PRT; 243 AA.
ID Q9BLR4;
AC Q9BLR4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell CLL/lymphoma 11A.
GN Bcl11a-L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;

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RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL: AK043677; BAC31616.1; --
SQ SEQUENCE 243 AA; 26823 MW; B19C19FD90473679 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 243;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CYTCKEPM TSA 14
Db 172 CTTCKQPFTA 182

RESULT 12
Q8L7L2 PRELIMINARY; PRT; 462 AA.
ID Q8L7L2;
AC Q8L7L2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE DNA-binding protein-like (Fragment).
GN AT5G47430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL ENBL: AY128390; AAM91593.1; --
DR InterPro; IPR001878; Znf_CCHC.
DR PRINTS; PR00939; C2HCZNFINGER.
KW DNA-binding.
FT NON TER 462
SQ SEQUENCE 462 AA; 50377 MW; 84EA259DFB3D564C CRC64;

Query Match 52.2%; Score 48; DB 10; Length 462;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELKCYCKEPM TSA 15
Db 292 ELKCPCKEVMKDA 306

RESULT 13
Q9H164 PRELIMINARY; PRT; 773 AA.
ID Q9H164;
AC Q9H164;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-cell lymphoma/leukaemia 11A long form.
GN BCL11A-L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Satterwhite E., Sonoki T., Willis T.G., Siebert R.;
RT "The BCL11 gene family: involvement of BCL11A in Hodgkin's and non-
Hodgkin's lymphomas.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ404612; CAC17724.1; -.
 DR InterPro; IPR007087; Znf C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR SMART; SM00355; Znf C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
 DR B-cell; Metal-binding; Zinc; Zinc-finger.
 KW B-cell; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 773 AA; 8393 MW; 1F8A6A0DBF45AB1E CRC64;

Query Match 52.2%; Score 48; DB 4; Length 773;
 Best Local Similarity 72.7%; Pred. No. 6.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
 ||||:||||
 Db 172 CTCKQP TSA 182

RESULT 14

QOQYE3 PRELIMINARY; PRT; 773 AA.
 AC QOQYE3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE C2H2-type zinc finger protein.
 GN BCL11A OR EVI9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BXH/2;
 RX MEDLINE=20221564; PubMed=10757802;
 RA Nakamura T., Yamazaki Y., Saiki Y., Moriyama M., Largaespada D.A.,
 RA Jenkins N.A., Copeland N.G.;
 RT "Evi9 encodes a novel zinc finger protein that physically interacts
 RT with BCL6, a known human B-cell proto-oncogene product."
 RL Mol. Cell. Biol. 20:3178-3186(2000).
 DR EMBL; AF051525; AAF22430.1; -.
 DR MGD; MGI:106190; Bcl11a.
 DR InterPro; IPR007087; Znf C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR SMART; SM00355; Znf C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 773 AA; 83855 MW; 3BD10B7F14AA9EC4 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 773;
 Best Local Similarity 72.7%; Pred. No. 6.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
 ||||:||||
 Db 172 CTCKQP TSA 182

RESULT 15

O9JIT4 PRELIMINARY; PRT; 776 AA.
 ID O9JIT4;
 AC O9JIT4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CTIP1 protein.
 GN BCL11A OR CTIP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP

SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=20209406; PubMed=10744719;
 RA Avram D., Fields A., Pretty On Top K., Nevriy D.J., Ishmael J.E.,
 RA Leid M.;
 RT "Isolation of a novel family of C(2)H(2) zinc finger proteins
 RT implicated in transcriptional repression mediated by chicken ovalbumin
 RT upstream promoter transcription factor (COUP-Tf) orphan nuclear
 RT receptors".
 RL J. Biol. Chem. 275:10315-10322(2000).
 DR EMBL; AF186018; AAF63682.1; -.
 DR MGD; MGI:106190; Bcl11a.
 DR InterPro; IPR007087; Znf C2H2.
 DR Pfam; PF00096; zf-C2H2; 3.
 DR SMART; SM00355; Znf C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 776 AA; 84116 MW; FBF388B7A03787A0 CRC64;

Query Match 52.2%; Score 48; DB 11; Length 776;
 Best Local Similarity 72.7%; Pred. No. 6.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CYTCKEPM TSA 14
 ||||:||||
 Db 172 CTCKQP TSA 182

Search completed: October 9, 2003, 14:11:55
 Job time : 99 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:04:11 ; Search time 23 Seconds
(without alignments)

32.714 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYTCCKEPMTSNAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	91.3	103	1 SLUR_HUMAN	P55000 homo sapien
2	47	51.1	110	1 SLUR_MOUSE	Q320K7 mus musculus
3	45	48.9	153	1 VE6_HPV10	P36809 human papil
4	44	47.8	126	1 CD59_RAT	P27274 rattus norv
5	44	47.8	224	1 MAUM_PARDE	Q51659 paracoccus
6	43	46.7	61	1 MT1A_HUMAN	P04731 homo sapien
7	43	46.7	154	1 VE6_HPV53	P36815 human papil
8	43	46.7	155	1 VE6_HPV56	P24836 human papil
9	43	46.7	295	1 EUTC_ECO57	Q8XEH3 escherichia
10	43	46.7	295	1 EUTC_ECOL6	Q8FIAL escherichia
11	43	46.7	295	1 EUTC_ECOL1	P19636 escherichia
12	43	46.7	365	1 P43_XENBO	P25066 xenopus bor
13	43	46.7	365	1 P43_XENLA	P25456 xenopus lae
14	43	46.7	469	1 APTD_DROME	P29673 drosophila
15	42	45.7	394	1 FDHB_MENTF	Q50570 methanobact
16	42	45.7	572	1 ZYX_HUMAN	Q15942 homo sapien
17	42	45.7	803	1 UBPE_YEAST	P18237 saccharomyc
18	41	44.6	126	1 CD59_PAPSP	Q28785 papio sp. (
19	41	44.6	149	1 VE6_HPV33	P06427 human papil
20	41	44.6	279	1 SLI3_MOUSE	Q70433 mus musculus
21	41	44.6	279	1 SLI3_RAT	Q35115 rattus norv
22	41	44.6	399	1 FDHB_METFO	P06130 methanobact
23	41	44.6	495	1 MLP2_DROME	Q24400 drosophila
24	41	44.6	3133	1 HMC7_BOMMO	P98092 bombyx mori
25	40	43.5	58	1 CTC7_HUMAN	Q9BQ22 homo sapien
26	40	43.5	61	1 MT1R_HUMAN	Q93083 homo sapien
27	40	43.5	61	1 MT2_CRIGR	P02799 cricetus
28	40	43.5	61	1 MT2_MESAU	P17808 mesocricetu
29	40	43.5	123	1 PSCA_HUMAN	Q43653 homo sapien
30	40	43.5	123	1 PSCA_MOUSE	P57096 mus musculus
31	40	43.5	128	1 CD59_CALSQ	P46657 callithrix
32	40	43.5	128	1 CD59_CERAE	Q28216 cercopithec
33	40	43.5	249	1 MOEB_SALTY	Q56067 salmonella

RESULT 1

SLUR_HUMAN

ID SLUR_HUMAN

AC P55000; Q92483; STANDARD; PRT; 103 AA.

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Secreted Ly-6/uPAR related protein 1 precursor (SLURP-1) (ARS

component B) (ARS(Component B)-81/S) (Anti-neoplastic urinary protein)

DE (ANUP).

GN SLURP1 OR ARS.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Mastrangeli R.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 22-36.

RC TISSUE=Granulocyte;

RX MEDLINE=96351837; PubMed=8742060;

RA Ridge R.O., Sloane N.H.;

RT "Partial N-terminal amino acid sequence of the anti-neoplastic

urinary protein (ANUP) and the anti-tumour effect of the N-terminal

nonapeptide of the unique cytokine present in human granulocytes.";

RN [3]

RP PARTIAL SEQUENCE.

RX MEDLINE=99226809; PubMed=10211827;

RA Andermann K., Wattler F., Wattler S., Heine G., Meyer M.,

RA Forsgmann W.-G., Nehls M.;

RT "Structural and phylogenetic characterization of human SLURP-1, the

first secreted mammalian member of the Ly-6/uPAR protein

superfamily.";

RN [4]

RL Protein Sci. 8:810-819(1999).

RX DISEASE.

RX MEDLINE=21181711; PubMed=11285253;

RA Fischer J., Bouadjir B., Hellig R., Huber M., Lefevre C., Jobard F.,

RA Macari F., Bakija-Konsuo A., Ait-Belkacem F., Weissenbach J.,

RA Lathrop M., Hohl D., Prud'homme J.-F.;

RT "Mutations in the gene encoding SLURP-1 in Mal de Meleda.";

RN Hum. Mol. Genet. 10:875-880(2001).

CC -1- FUNCTION: Has an antitumor activity.

CC -1- SUBUNIT: Homodimer.

CC -1- TISSUE SPECIFICITY: GRANULOCYTES. EXPRESSED IN SKIN.

CC -1- DISEASE: Defects in SLURP1 are a cause of Mal de Meleda (MDM), a

rare autosomal recessive skin disorder, characterized by

transgressive palmo-plantar keratoderma (PPK), keratotic skin

lesions, perioral erythema, brachydactyly and nail abnormalities.

CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.

CC -1- CAUTION: IT IS NOT CERTAIN THAT ARS AND ANUP ARE IDENTICAL


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RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC -----
DR EMBL; X74474; CAAS2543.1; --
DR PIR; S36503; S36503; E6.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger.
FT ZN FING 33 69 POTENTIAL.
FT ZN FING 106 142 POTENTIAL.
SQ SEQUENCE 153 AA; 18266 MW; F7295E15261FC433 CRC64;

Query Match 48.9%; Score 45; DB 1; Length 153;
Best Local Similarity 45.5%; Pred. No. 2.2;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKCYCKEPMPT 12
Db 104 IRCYRCQPLT 114

RESULT 4
CD59 RAT
ID CD59_RAT STANDARD; PRT; 126 AA.
AC P27274;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN CD59.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.; AND SEQUENCE OF 23-64.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95091697; PubMed=7528012;
RA Rushmere N.K., Harrison R.A., van den Berg C.W., Morgan B.P.;
RT "Molecular cloning of the rat analogue of human CD59: structural
RT comparison with human CD59 and identification of a putative active
RT site.";
RL Biochem. J. 304:595-601(1994).
RN [2]
RP SEQUENCE OF 23-37.
RC TISSUE=Erythrocyte;
RX MEDLINE=92286999; PubMed=1376109;
RA Hughes T.R., Piddlesden S.J., Williams J.D., Harrison R.A.,
RA Morgan B.P.;
RT "Isolation and characterization of a membrane protein from rat
RT erythrocytes which inhibits lysis by the membrane attack complex of
RT rat complement.";
RL Biochem. J. 284:169-176(1992).
CC -1- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC
CC ASSEMBLY.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- PTM: N-GLYCOSYLATED.

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CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC -----
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CC -----
DR EMBL; U48255; AAA88909.1; --
DR PIR; S53340; S53340.
DR HSPSP; P13987; ICDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR LY6; 1.
DR ProDom; PD003128; Ly-6 CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; 1.
KW Antigen; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 22
FT CHAIN 23 101 CD59 GLYCOPROTEIN.
FT PROPEP 102 126 REMOVED IN MATURE FORM (BY SIMILARITY).
FT LIPID 101 101 GPI-ANCHOR (BY SIMILARITY).
FT DOMAIN 23 110 UPAR/LY6.
FT DISULFID 25 48 BY SIMILARITY.
FT DISULFID 28 35 BY SIMILARITY.
FT DISULFID 41 61 BY SIMILARITY.
FT DISULFID 67 85 BY SIMILARITY.
FT DISULFID 86 91 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 126 AA; 13790 MW; 54B9C58AB2073005 CRC64;

Query Match 47.8%; Score 44; DB 1; Length 126;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYCKEPMPT 13
Db 23 LRCYNCLDPVSS 34

RESULT 5
MAUM FARDE
ID MAUM FARDE STANDARD; PRT; 224 AA.
AC Q51659;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methylamine utilization ferredoxin-type protein maum precursor.
GN MAUM.
OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=266;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pd 1222;
RX MEDLINE=95324575; PubMed=7601147;
RA van der Palen C.J., Slotboom D.J., Jongejan L., Reijnders W.N.,
RA Harms N., Duine J.A., van Spanning R.J.;
RT "Mutational analysis of mau genes involved in methylamine metabolism
RT in Paracoccus denitrificans.";
RL Eur. J. Biochem. 230:860-871(1995).
CC -1- FUNCTION: INVOLVED IN ELECTRON TRANSFER (POTENTIAL).
CC -1- PATHWAY: Methylamine utilization.
CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
CC 'BACTERIAL-TYPE' 4Fe-4S FERREDOXINS.
CC -----
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CC EMBL; U15028; AA86468.1; -.
CC PIR; S65960; S65960.
CC InterPro; IPR001450; 4Fe4S_ferredoxin.
CC InterPro; IPR004494; MauM_NapG.
CC InterPro; IPR006311; Tat.
CC Pfam; PF00037; fer4; 2.
CC TIGRFAMs; TIGR00397; mauM_napG; 1.
CC TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
CC PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
KW Electron transport; Iron-sulfur; 4Fe-4S; Signal.
FT SIGNAL 1 41
FT CHAIN 42 224
FT METAL 64 64
FT METAL 67 67
FT METAL 70 70
FT METAL 74 74
FT METAL 102 102
FT METAL 105 105
FT METAL 110 110
FT METAL 114 114
FT METAL 142 142
FT METAL 150 150
FT METAL 153 153
FT METAL 157 157
FT METAL 186 186
FT METAL 189 189
FT METAL 192 192
FT METAL 196 196
SQ SEQUENCE 224 AA; 23694 MW; F7758CA696293F37 CRC64;

Query Match 47.8%; Score 44; DB 1; Length 224;
Best Local Similarity 43.8%; Pred. No. 4.6;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ELKCYCTCKEPTMTSAAC 16
Db 99 EVPCYCKDVPFCARAC 114

RESULT 6
MT1A HUMAN STANDARD; PRT; 61 AA.
AC P04731;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metallothionein-IA (MT-IA).
GN MT1A.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84205649; PubMed=6327055;
RA Richards R.I., Heguy A., Karin M.;
RT "Structural and functional analysis of the human metallothionein-IA
RL gene: differential induction by metal ions and glucocorticoids.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
CC GLUCOCORTICOID.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS;
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
CC -----
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CC -----
CC EMBL; K01383; AAA59586.1; -.
CC EMBL; BC029475; AAH29475.1; -.
CC PIR; A24502; SMHUIA.
CC HSP; P02795; 1MHU.
CC Genew; HGNC:7393; MT1A.
CC MIM; 156350; -.
CC GO; GO:0005737; Cytoplasm; NAS.
CC GO; GO:0005508; F: copper/cadmium binding; NAS.
CC GO; GO:0008270; F: zinc ion binding activity; NAS.
CC InterPro; IPR003019; Metallothion.
CC InterPro; IPR000006; Metallothion_1.
CC Pfam; PF00131; metalthio; 1.
CC PRINTS; PR00860; MTVEBERATE.
CC PROSITE; PS00203; METALLOTHIONEIN VRT; 1.
CC Metal-binding; Metal-thiolate cluster; Zinc; Copper; Cadmium;
CC Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 1 29 BETA.
FT DOMAIN 30 61 ALPHA.
FT METAL 5 5 CLUSTER B.
FT METAL 7 7 CLUSTER B.
FT METAL 13 13 CLUSTER B.
FT METAL 15 15 CLUSTER B.
FT METAL 19 19 CLUSTER B.
FT METAL 21 21 CLUSTER B.
FT METAL 24 24 CLUSTER B.
FT METAL 26 26 CLUSTER B.
FT METAL 29 29 CLUSTER B.
FT METAL 33 33 CLUSTER A.
FT METAL 34 34 CLUSTER A.
FT METAL 36 36 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT METAL 41 41 CLUSTER A.
FT METAL 44 44 CLUSTER A.
FT METAL 48 48 CLUSTER A.
FT METAL 50 50 CLUSTER A.
FT METAL 57 57 CLUSTER A.
FT METAL 59 59 CLUSTER A.

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OX NCBI_TaxID=10596;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90063558; PubMed=2555440;
RA Leorincz A.T., Quinn A.P., Goldeborough M.D., McAllister P.,
RA Temple G.P.;
RA "Human papillomavirus type 56: a new virus detected in cervical
RT cancers";
RL J. Gen. Virol. 70:3099-3104(1989).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RA "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -!- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74483; CAA52596.1; --
DR PIR; A33377; W6WL56
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;
KW Oncogene.
FT ZN FING 33 69
FT ZN FING 106 142
FT ZN FING 106 142
SQ SEQUENCE 155 AA; 18524 MW; E8732949398B4C4B CRC64;
Query Match 46.7%; Score 43; DB 1; Length 155;
Best Local Similarity 45.5%; Pred. No. 4.6;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 2 LKYCTCKEPMPT 12
DB 104 IRCYRCQSPLT 114
::|||::|:|
RESULT 9
EUTC_ECO57
ID EUTC_ECO57 STANDARD; PRT; 295 AA.
OC O8XSE3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine
DE ammonia-lyase small subunit).
GN EUTC OR Z3705 OR ECS3311.
GN Escherichia coli O157:H7.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11208551;
RA Ferna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT

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RN RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasekawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin (By similarity).
CC -!- PATHWAY: Ethanolamine utilization.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -!- SIMILARITY: Belongs to the eutC family.
CC
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CC
DR EMBL; AE005474; AAG57558.1; -.
DR EMBL; AP002561; BAB36734.1; -.
DR PIR; B85887; B85887.
DR PIR; G91042; G91042.
DR HAWAP; MF 00601; -.
DR Lyase; Cofact; Complete proteome.
KW CONFLICT 82 82 R -> H (IN REF. 2).
FT SEQUENCE 295 AA; 31812 MW; 3D55EAD80374A1D CRC64;
SQ
Query Match 46.7%; Score 43; DB 1; Length 295;
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 9; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
Qy 1 ELKC--YTCPEPMTSAAC 16
Db 26 EAKCATTTCAAPVTSESC 43
RESULT 10
EUTC_ECOL6
ID EUTC_ECOL6 STANDARD; PRT; 295 AA.
AC Q8PFA1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine
DE ammonia-lyase small subunit).
GN EUTC OR C2974.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22398234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roessch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RA "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin (By similarity).
CC -!- PATHWAY: Ethanolamine utilization.
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By

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CC similarity).
CC -!- SIMILARITY: Belongs to the eutC family.
CC
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CC
DR EMBL; AE016764; AAN81424.1; -.
DR HAWAP; MF 00601; -.
DR Lyase; Cofact; Complete proteome.
SQ SEQUENCE 295 AA; 31811 MW; B07601450F8B20EA CRC64;
Query Match 46.7%; Score 43; DB 1; Length 295;
Best Local Similarity 50.0%; Pred. No. 8.6;
Matches 9; Conservative 2; Mismatches 5; Indels 2; Gaps 1;
Qy 1 ELKCVT--CKEPMTSAAC 16
Db 26 EAKCATTTCAAPVTSESC 43
RESULT 11
EUTC_ECOL1
ID EUTC_ECOL1 STANDARD; PRT; 295 AA.
AC P19636; P78273;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine
DE ammonia-lyase small subunit).
GN EUTC OR B2440.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayaashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satchi Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yanagata S., Horiuchi T.;
RA "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [3]
RP SEQUENCE OF 1-15.
RX MEDLINE=90324235; PubMed=2197274;
RA Faust L.R.P., Connor J.A., Roof D.M., Hoch J.A., Babor B.M.;
RA "Cloning, sequencing, and expression of the genes encoding the
RT adenosylcobalamin-dependent ethanolamine ammonia-lyase of Salmonella
RT typhimurium";
RL J. Biol. Chem. 265:12462-12466(1990).
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).
CC -!- COFACTOR: Adenosylcobalamin.

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DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
KW Zinc-finger; Metal-binding; RNA-binding; Repeat.
FT ZN_FING 15 39 C2H2-TYPE 1.
FT ZN_FING 45 69 C2H2-TYPE 2.
FT ZN_FING 75 100 C2H2-TYPE 3.
FT ZN_FING 106 130 C2H2-TYPE 4.
FT ZN_FING 136 160 C2H2-TYPE 5.
FT ZN_FING 163 187 C2H2-TYPE 6.
FT ZN_FING 191 213 C2H2-TYPE 7.
FT ZN_FING 220 245 C2H2-TYPE 8.
FT ZN_FING 251 275 C2H2-TYPE 9.
SQ SEQUENCE 365 AA; 41726 MW; D7E8C765B0E42BF2 CRC64;

Query Match 46.7%; Score 43; DB 1; Length 365;
Best Local Similarity 46.7%; Pred No. 11;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAA 15
||| ||| |:
DB 190 ELQCAACKPFKKAS 204

RESULT 13
P43_XENLA
ID P43_XENLA STANDARD; PRT; 365 AA.
AC P25456;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE P43 5S RNA binding protein (42S P43) (Thesaurin B).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235278; PubMed=2331751;
RA Joho K.E., Darby M.K., Crawford E.T., Brown D.D.;
RT "A finger protein structurally similar to TFIIIA that binds
exclusively to 5S RNA in Xenopus.";
RL Csil 61:293-300(1990).
CC -|- FUNCTION: P43 IS A 5S RNA BINDING PROTEIN WHICH IS A MAJOR
CONSTITUENT OF OOCYTES AND COMPRISES PART OF A 42S
RIBONUCLEOPROTEIN STORAGE PARTICLE.
CC -|- SUBUNIT: THE 42S RNP PARTICLE COMPRISES FOUR SUBUNITS EACH OF
WHICH CONTAINS ONE MOLECULE OF 5S RNA, THREE MOLECULES OF TRNA,
TWO MOLECULES OF P50 (EF1-ALPHA) AND ONE MOLECULE OF THE 5S RNA
BINDING PROTEIN 43.
CC -----
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CC -----
DR ENBL; M22473; AAA49714.1; -.
DR HSSP; P03001; 1TF3.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 9.
DR SMART; SM00355; Znf_C2H2; 9.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
KW Zinc-finger; Metal-binding; RNA-binding; Repeat.
FT ZN_FING 15 39 C2H2-TYPE.
FT ZN_FING 45 69 C2H2-TYPE.
FT ZN_FING 75 100 C2H2-TYPE.
FT ZN_FING 106 130 C2H2-TYPE.
FT ZN_FING 136 160 C2H2-TYPE.
FT ZN_FING 163 187 C2H2-TYPE.
FT ZN_FING 191 213 C2H2-TYPE.
FT ZN_FING 220 245 C2H2-TYPE.

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FT  ZN FING      220   245      C2H2-TYPE.
FT  ZN FING      251   275      C2H2-TYPE.
SQ  SEQUENCE     365 AA;  41694 MW;  2B5B5E66D7192995 CRC64;

Query Match      46.7%; Score 43; DB 1; Length 365;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY  1 ELKCYTCCKEPTMSAA 15
    ||| ||| |||
Db  190 ELQCAACKPKPKAS 204

RESULT 14
APTE DROME
ID  APTE DROME      STANDARD;      PRT;      469 AA.
AC  P29673; Q9V9H5;
DT  01-APR-1993 (Rel. 25, Created)
DT  01-APR-1993 (Rel. 25, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Apterous protein.
GN  AP OR CG8376.
OS  Drosophila melanogaster (Fruit fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92249766; PubMed=1349545;
RA  Cohen B., McGuffin M.E., Pfeifle C., Segal D., Cohen S.M.;
RT  "Apterous, a gene required for imaginal disc development in
RT  Drosophila encodes a member of the LIM family of developmental
RT  regulatory proteins.";
RL  Genes Dev. 6:715-729 (1992).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92398973; PubMed=1524829;
RA  Bourguin C., Lundgren S.E., Thomas J.B.;
RT  "Apterous is a Drosophila LIM domain gene required for the
RT  development of a subset of embryonic muscles.";
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Berkely;
RX  MEDLINE=20196006; PubMed=10731132;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Borchan M.R., Bouck J., Brockstein P., Brotter P.,
RA  Burtis K., Busam D.A., Butler H., Cantarel D., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glisdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jallali M., Kaulush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei E., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
CC  -1- FUNCTION: REQUIRED FOR THE NORMAL DEVELOPMENT OF THE WING AND
CC  HALTER IMAGINAL DISKS.
CC  -1- SUBCELLULAR LOCATION: Nuclear.
CC  -1- TISSUE SPECIFICITY: EXPRESSED IN PNS AND CNS.
CC  -1- SIMILARITY: Contains 1 homeobox domain.
CC  -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  ENBL; X65158; CAA46276.1; -
DR  ENBL; M92841; AAA28673.1; -
DR  ENBL; A8003785; AAM68357.1; -
DR  PIR; JH0718; JH0718.
DR  HSP; P32965; ICTL.
DR  TRANSFAC; T01074; -
DR  FlyBase; FBgn0000099; ap.
DR  GO; GO:0005634; C:nucleus; IDA.
DR  GO; GO:0007411; P:axon guidance; IMP.
DR  GO; GO:0007559; P:histolysis; IMP.
DR  GO; GO:0007479; P:leg disc proximal/distal pattern formation; IMP.
DR  GO; GO:0007517; P:leg disc development; IMP.
DR  GO; GO:0007399; P:neurogenesis; IMP.
DR  GO; GO:0006350; P:transcription; IMP.
DR  InterPro; IPR001356; Homeobox.
DR  InterPro; IPR001781; LIM.
DR  Pfam; PF00046; homeobox; 1.
DR  Pfam; PF00412; LIM; 2.
DR  ProDom; PD000010; Homeobox; 1.
DR  ProDom; PD000094; LIM; 2.
DR  SMART; SM00389; HOX; 1.
DR  SMART; SM00132; LIM; 2.
DR  PROSITE; PS00478; LIM DOMAIN 1; 2.
DR  PROSITE; PS00023; LIM DOMAIN 2; 2.
DR  PROSITE; PS00027; HOMEBOX 1; 1.
DR  PROSITE; PS00071; HOMEBOX 2; 1.
KW  Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW  Repeat; LIM domain; Metal-binding; Zinc.
FT  DOMAIN 148 200 LIM 1.
FT  DOMAIN 210 263 LIM 2.
FT  DNA BIND 367 426 HOMEBOX
SQ  SEQUENCE 469 AA; 52053 MW; FA9B43B8C7B9B22D CRC64;

Query Match      46.7%; Score 43; DB 1; Length 469;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY  2 LKCYTCCKEPM 11
    ||| ||| |||
Db  173 LQCYACROPL 182

RESULT 15
EDHB METTF
ID  FDHB METTF STANDARD; PRT; 394 AA.
AC  Q50570;

```

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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Formate dehydrogenase beta chain (EC 1.2.1.2).
GN FDHB.
OS Methanobacterium thermoformicicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3720 / Z-245;
RX MEDLINE=97158688; PubMed=9006048;
RA Noelling J., Reeve J.N.;
RT "Growth- and substrate-dependent transcription of the formate
dehydrogenase (fdhCAB) operon in Methanobacterium thermoformicum Z-
245."
RL J. Bacteriol. 179:899-908(1997).
CC -!- FUNCTION: M.THERMOFORMICICUM USE THE FDH ENZYME TO GROW ON
FORMATE.
CC -!- CATALYTIC ACTIVITY: Formate + NAD(+) = CO(2) + NADH.
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (PROBABLE).
CC -!- SUBUNIT: Dimer of alpha and beta chains.
CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
CC -!- SIMILARITY: STRONG, TO THE BETA SUBUNIT OF M.THERMOAUTOTROPHICUM
FDH.
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-----
CC EMBL; U52681; AAC44821.1; -.
CC HSP; Q45560; LBWE.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 1.
DR Pfam; PF04432; FthB_FdhB_C; 1.
DR Pfam; PF04432; FthB_FdhB_N; 1.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 2.
KW Oxidoreductase; NAD; Electron transport; Iron-sulfur; 4Fe-4S.
FT METAL 295 295 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 298 298 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 301 301 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 305 305 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 346 346 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 349 349 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 352 352 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 356 356 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 394 AA; 43683 MW; F95B3E85B4C44316 CRC64;
Query Match 45.7%; Score 42; DB 1; Length 394;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 2 LKCYTCKEPMTSAAC 16
Db 296 IKCYSCREACPICYC 310
:|:|:|:|

```

Search completed: October 9, 2003, 14:10:10
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:07:37 ; Search time 39 Seconds
(without alignments)
39.454 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYCKEPTMSAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	91.3	103	2 A59031	ARS component B 81
2	58	63.0	15	2 A58945	anti-neoplastic ur
3	46	50.0	225	2 A69305	conserved hypothet
4	45	48.9	153	2 S36503	E6 protein - human
5	45	48.9	157	2 F69368	Carbon monoxide de
6	44	47.8	126	2 S53340	CD59 protein - rat
7	44	47.8	134	2 D45835	Ly6 homolog RK3 pr
8	44	47.8	224	2 S65960	mauM protein precu
9	44	47.8	388	2 T43019	probable DNA-bindi
10	44	47.8	391	2 E83840	hypothetical prote
11	44	47.8	580	2 S13328	hypothetical prote
12	43	46.7	61	1 SMH01A	metallothionein IA
13	43	46.7	114	2 AF2315	hypothetical prote
14	43	46.7	154	2 S36527	E6 protein - human
15	43	46.7	155	1 W6WL56	E6 protein - human
16	43	46.7	295	2 G65018	ethanolamine ammon
17	43	46.7	295	2 G91042	ethanolamine ammon
18	43	46.7	295	2 B85887	ethanolamine ammon
19	43	46.7	365	2 C34895	SS RNA-binding pro
20	43	46.7	365	2 A34895	SS RNA-binding pro
21	43	46.7	469	1 JH0718	homeotic protein a
22	43	46.7	1322	2 T15689	hypothetical prote
23	42	45.7	71	2 B69428	hypothetical prote
24	42	45.7	572	2 G02845	zyxin - human
25	42	45.7	761	2 T33816	hypothetical prote
26	42	45.7	803	2 S45916	hypothetical prote
27	41	44.6	32	2 S19906	E6-II protein - hu
28	41	44.6	35	2 S19909	E6-III protein - h
29	41	44.6	47	2 S21825	E6-I protein - hum

CD59 protein - bab
E6 protein - human
hypothetical 22.8K
R01H10.4 protein (
hypothetical prote
formate dehydrogen
hypothetical prote
hypothetical prote
hypothetical prote
retinoblastoma bin
proliferation pote
hemocytin - silkw
hypothetical prote
metallothionein II
metallothionein IR
metallothionein II

ALIGNMENTS

RESULT 1

A59031

ARS component B 81/S protein precursor - human

N;Alternate names: secreted Ly-6/uPAR related protein 1; SLURP-1

C;Species: Homo sapiens (man)

C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 29-Oct-1999

C;Accession: A59031; A58842

R;Mastrangeli, R.

submitted to the EMBL Data Library, August 1996

A;Description: ARS gene, component B.

A;Reference number: A59031

A;Accession: A59031

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-103 <MAS>

A;Cross-references: GB:X99977; NID:gl536901; PIDN:CAA68237.1; PID:c26523; PID:gl536902

A;Experimental source: placenta

R;Ademann, K.; Wattler, F.; Wattler, S.; Heine, G.; Meyer, M.; Forssmann, W.G.; Nehls,

submitted to the Protein Sequence Database, July 1998

A;Description: Secreted protein, related to Ly-6, uPAR, soluble CD59, and snake and fro

A;Reference number: A58842

A;Accession: A58842

A;Molecule type: protein

A;Residues: 23-103 <ADE>

C;Genetics:

A;Gene: ARS

A;Introns: 20/1; 60/1

C;Keywords: glycoprotein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-22/Domain: propeptide #status predicted <PRO>

F;23-103/Product: ARS component B 81/S protein #status experimental <MAT>

F;25-50,28-37,94-99/Disulfide bonds: #status experimental

F;43-77,73-93/Disulfide bonds: (or 43-73, 77-93) #status experimental

F;64/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 91.3%; Score 84; DB 2; Length 103;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYCKEPTMSAAC 16

DB 23 LKCYCKEPTMSASC 37

RESULT 2

A58945

anti-neoplastic urinary protein - human (fragment)

N;Alternate names: ANUP

C;Species: Homo sapiens (man)

C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Apr-1999

C;Accession: A58945

R;Ridge, R.J.; Sloane, N.H.

Db 104 IRCYRCQOPLT 114

RESULT 5
F69368

carbon monoxide dehydrogenase, iron sulfur subunit (cooF) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C:Accession: F69368

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, J.; Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Pyrococcus furiosus
A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: F69368

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-157 <KLE>

A:Cross-references: GB:AE001038; GB:AE000782; NID:q2689361; PIDN:AA890290.1; PID:q26494

C:Superfamily: nrfC protein; ferredoxin 2 [4Fe-4S] homology

F:92-152/Domain: ferredoxin 2 [4Fe-4S] homology <FER1>

Query Match 48.9%; Score 45; DB 2; Length 157;
Best Local Similarity 53.3%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 LKCYTCKEPMTSAAC 16

Db 66 LQCRHCEPRKVAAC 80

RESULT 6
S53340

CD59 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999

C:Accession: S53339

R:Rushmere, N.K.; Harrison, R.A.; van den Berg, C.W.; Morgan, B.P. Biochem. J. 304, 593-601, 1994

A:Title: Molecular cloning of the rat analogue of human CD59: structural comparison with mouse CD59

A:Reference number: S53339; MUID:95091697; PMID:7528012

A:Accession: S53340

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-126 <RUS>

A:Cross-references: GB:U48255; NID:g1199654; PIDN:AAA88909.1; PID:g1199655

A:Accession: S53339

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-24, 'X', 26-27, 'X', 36-37, 'X', 39-40, 'X', 42-47, 'X', 49-58, 'X', 60, 'E', 62

C:Superfamily: Ly-6 antigen; Ly-6 homology

F:23-101/Domain: Ly-6 homology <LY6>

Query Match 47.8%; Score 44; DB 2; Length 126;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LKCYTCKEPMTS 13

Db 23 LRCYNCLDPVSS 34

RESULT 7
D45835

Ly6 homolog RK3 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 31-Jan-2000

C:Accession: D45835; C45835

R:Friedman, S.; Palfree, R.G.E.; Sirlin, S.; Haemmerling, U. Immunogenetics 31, 104-111, 1990

A;Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidney
 A;Reference number: A45835; MUID:90152758; PMID:2154400

A;Accession: D45835
 A;Molecule type: mRNA
 A;Residues: 1-134 <FRI>

A;Cross-references: GB:M30690; NID:g205249; PIDN:AAA41547.1; PID:g205250

A;Experimental source: clone RK3

A;Accession: C45835

A;Molecule type: mRNA

A;Residues: 2-134 <FR2>

A;Cross-references: GB:M30691; NID:g205251; PIDN:AAA41548.1; PID:g205252

A;Experimental source: clone RK11

C;Superfamily: Ly-6 antigen; Ly-6 homology

C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linked

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-105/Product: Ly6 homolog RK3 #status predicted <MAT>

F;106-134/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F;105/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match 47.8%; Score 44; DB 2; Length 134;

Best Local Similarity 53.3%; Pred. No. 14;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16

|||||:|:|:|

Db 27 LKCYSCIEVPLNANC 41

|||||:|:|:|

RESULT 8

S65960

C;Superfamily: maum protein precursor - Paracoccus denitrificans

C;Species: Paracoccus denitrificans

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999

C;Accession: S65960

R;van der Palen, C.J.N.M.; Slotboom, D.J.; Jongejan, L.; Reijnders, W.N.M.; Harms, N.; D

Eur. J. Biochem. 230, 860-871, 1995

A;Title: Mutational analysis of mau genes involved in methylamine metabolism in Paracoccus

A;Reference number: S65958; MUID:95324575; PMID:7601147

A;Accession: S65960

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-224 <VAN>

A;Cross-references: EMBL:U15028; NID:g595839; PIDN:AAA86468.1; PID:g595842

C;Genetics:

A;Gene: maum

C;Superfamily: conserved hypothetical protein H10345; ferredoxin 2 [4Fe-4S] homology

F;1-46/Domain: signal sequence #status predicted <SIG>

F;47-224/Product: maum protein #status predicted <MAT>

F;57-122/Domain: ferredoxin 2 [4Fe-4S] homology <FER6>

Query Match 47.8%; Score 44; DB 2; Length 224;

Best Local Similarity 43.8%; Pred. No. 21;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAAC 16

|||||:|:|:|

Db 99 EVPCYMKDVPFCARAC 114

|||||:|:|:|

RESULT 9

T43019

C;Superfamily: probable DNA-binding protein - African malaria mosquito retrotransposon Q retrotransposon

C;Species: Anopheles gambiae (African malaria mosquito)

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C;Accession: T43019

R;Besansky, N.J.; Bedell, J.A.; Mukabayire, O.

Insect Mol. Biol. 3, 49-56, 1994

A;Title: Q: a new retrotransposon from the mosquito Anopheles gambiae.

A;Reference number: 222286; MUID:94348637; PMID:8069416

A;Accession: T43019

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-388 <BES>

Query Match 47.8%; Score 44; DB 2; Length 580;

Best Local Similarity 53.8%; Pred. No. 45;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAAC 16

|||||:|:|:|

Db 418 CVVCSEPTTANC 430

|||||:|:|:|

RESULT 12

SMHUIA

metallothionein 1A - human

A;Cross-references: EMBL:U03849; NID:g432429; PID:g577351; PIDN:AAAS3488.1

A;Experimental source: strain G3; clone Q-22

C;Genetics:

A;Mobile element: retrotransposon Q

Query Match 47.8%; Score 44; DB 2; Length 388;

Best Local Similarity 38.5%; Pred. No. 33;

Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAAC 16

|||||:|:|:|

Db 16 CFSCAEPLATGC 28

|||||:|:|:|

RESULT 10

E83840

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: E83840

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: E83840

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-391 <STO>

A;Cross-references: GB:AP001512; GB:BA000004; NID:gl0174030; PIDN:BA805244.1; GSPDB:GNO

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1525

Query Match 47.8%; Score 44; DB 2; Length 391;

Best Local Similarity 43.8%; Pred. No. 33;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELKCYTCKEPMTSAAC 16

|||||:|:|:|

Db 267 ETTCAQCRTPMKGSAC 282

|||||:|:|:|

RESULT 11

S13328

C;Species: Drosophila melanogaster

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997

C;Accession: S13328

R;O'Hare, K.; Alley, M.R.K.; Cullingford, T.E.; Driver, A.; Sanderson, M.J.

Mol. Gen. Genet. 225, 17-24, 1991

A;Title: DNA sequence of the Doc retroposon in the white-one mutant of Drosophila melan

A;Reference number: S13328; MUID:91155930; PMID:1705654

A;Accession: S13328

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-580 <MOL>

A;Cross-references: EMBL:X17551

C;Genetics:

A;Gene: FlyBase:Doc

A;Cross-references: FlyBase:FBgn0000481

Query Match 47.8%; Score 44; DB 2; Length 580;

Best Local Similarity 53.8%; Pred. No. 45;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAAC 16

|||||:|:|:|

Db 418 CVVCSEPTTANC 430

|||||:|:~|:|

RESULT 12

SMHUIA

metallothionein 1A - human

C:Species: Homo sapiens (man)
C:Date: 24-Jun-1987 #sequence_revision 09-Sep-1994 #text_change 22-Jun-1999
C:Accession: A24502
R:Richards, R.I.; Heguy, A.; Karin, M.
Cell 37, 263-272, 1984
A:Title: Structural and functional analysis of the human metallothionein-IA gene: differed
A:Reference number: A24502; MUID:84205649; PMID:6327055
A:Accession: A24502
A:Molecule type: DNA
A:Residues: 1-61 <RIC>
A:Cross-references: GB:K01383; NID:gl87536; PIDN:AAA59586.1; PID:g386864
C:Genetics:
A:Gene: GDB:MT1A; MT1
A:Cross-references: GDB:125559; OMIM:156350
A:Map position: 16q13-16q13
A:Introns: 10/1; 32/1
C:Superfamily: metallothionein
C:Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
F:1-29/Domain: beta <NH2>
F:30-61/Domain: alpha <ALP>
F:1/Modified site: acetylated amino end (Met) #status predicted
F:5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F:33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre

Query Match 46.7%; Score 43; DB 1; Length 61;
Best Local Similarity 40.9%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 ELKCVTCKE-----PMTSAAC 16
DB 23 ECKNSCKKSCCSCCPMSCAKC 44

RESULT 13
AF2315
hypothetical protein alr4077 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120 [imported]
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AF2315
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2315
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-114 <KUP>
A:Cross-references: GB:BA000019; PIDN:BA875776.1; PID:gl7133212; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4077

Query Match 46.7%; Score 43; DB 2; Length 114;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 CYTCKEPMTSAA 15
DB 36 CYTCGQDQNSAS 47

RESULT 14
S36527
E6 protein - human papillomavirus type 53
C:Species: human papillomavirus type 53
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36527
R:Deilius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469

A:Accession: S36527
A:Molecule type: DNA
A:Residues: 1-154
A:Cross-references: EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397047
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 46.7%; Score 43; DB 2; Length 154;
Best Local Similarity 45.5%; Pred. No. 22;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
DB 105 IRCVRCQHPLT 115

RESULT 15
W6WL56
E6 protein - human papillomavirus type 56
C:Species: human papillomavirus type 56
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999
C:Accession: A33377; S36579
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A:Reference number: A33377; MUID:90063558; PMID:2555440
A:Accession: A33377
A:Molecule type: DNA
A:Residues: 1-155 <LOE>
R:Deilius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36579
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-155 <DBL>
A:Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:33-69/Region: zinc finger CCCC motif
F:106-142/Region: zinc finger CCCC motif

Query Match 46.7%; Score 43; DB 1; Length 155;
Best Local Similarity 45.5%; Pred. No. 22;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMT 12
DB 104 IRCVRCQSPLT 114

Search completed: October 9, 2003, 14:12:39
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:09:47 ; Search time 26 Seconds
(without alignments)
99.156 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 LKCYCKEPMPTSAAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	94.6	16	8	US-08-986-606C-1
2	58	63.0	558	9	Sequence 1, Appli
3	50	54.3	212	15	Sequence 47724, A
4	50	54.3	272	15	Sequence 49, Appl
5	50	54.3	612	12	Sequence 36, Appl
6	48	52.2	270	10	Sequence 90, Appl
7	48	52.2	293	9	Sequence 1433, Ap
8	46	50.0	125	10	Sequence 1119, Ap
9	46	50.0	125	10	Sequence 454, App
10	46	50.0	125	10	Sequence 454, App
11	46	50.0	125	10	Sequence 454, App
12	46	50.0	125	10	Sequence 454, App
13	46	50.0	125	11	Sequence 454, App
14	46	50.0	125	11	Sequence 454, App
15	46	50.0	125	11	Sequence 454, App

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16 46 50.0 125 11 US-09-978-403A-454 Sequence 454, App
17 46 50.0 125 11 US-09-978-564A-454 Sequence 454, App
18 46 50.0 125 11 US-09-999-833A-454 Sequence 454, App
19 46 50.0 125 11 US-09-981-915A-454 Sequence 454, App
20 46 50.0 125 11 US-09-978-824-454 Sequence 454, App
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33 46 50.0 125 12 US-10-017-083A-454 Sequence 454, App
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35 46 50.0 125 12 US-10-216-163-140 Sequence 454, App
36 46 50.0 125 12 US-10-145-128A-454 Sequence 140, App
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42 46 50.0 125 12 US-10-145-017A-454 Sequence 454, App
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44 46 50.0 125 12 US-10-165-067A-454 Sequence 454, App
45 46 50.0 125 12 US-10-218-765-140 Sequence 140, App

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ALIGNMENTS

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RESULT 1
US-08-986-606C-1
; Sequence 1, Application US/08986606C
; Publication No. US20020061851A1
; GENERAL INFORMATION:
; APPLICANT: Sloane, Nathan H
; TITLE OF INVENTION: Sixteen Amino Acid of the Antineoplastic Protein (ANUP)
; TITLE OF INVENTION: as a Pharmaceutically Active Anti-Tumor Agent
; FILE REFERENCE: 99181
; CURRENT APPLICATION NUMBER: US/08/986,606C
; CURRENT FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; LOCATION: 1
; OTHER INFORMATION: Xaa is -N-Terminal pyrroglutamyl (pyroGLU)
; OTHER INFORMATION: Description of Artificial Sequence, the partial N-terminal
; OTHER INFORMATION: amino acid sequence of the Antineoplastic Protein (ANUP)
US-08-986-606C-1

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Query Match          94.6%; Score 87; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 LKCYCKEPMPTSAAC 16
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Db 2 LKCYCKEPMPTSAAC 16
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RESULT 2
US-09-864-761-47724
; Sequence 47724, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

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; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
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; SEQ ID NO 47724
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; OTHER INFORMATION: MAP TO AC011451.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: P51523, EVALUATE 0.00e+00
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Db 285 KVCYCKGKPTSSAC 298
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US-10-091-458-49
; Sequence 49, Application US/10091458
; Publication No. US20030068627A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT206C1
; CURRENT APPLICATION NUMBER: US/10/091,458
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
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; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
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; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08

Query Match 54.3%; Score 50; DB 15; Length 212;
Best Local Similarity 53.8%; Pred. No. 4.3;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTMTSAAC 16
|:|:|:|:|:|:|
Db 172 CFTCQETPTSTGC 184

RESULT 4
US-10-091-458-36
; Sequence 36, Application US/10091458
; Publication No: US20030068627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ06C1
; CURRENT APPLICATION NUMBER: US/10/091,458
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,900
; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
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; PRIOR FILING DATE: 2000-08-22
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; PRIOR FILING DATE: 2000-08-14
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; PRIOR APPLICATION NUMBER: 60/241,809
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 ; PRIOR APPLICATION NUMBER: 60/249,264
 ; PRIOR FILING DATE: 2000-11-17
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 ; PRIOR FILING DATE: 2000-09-08
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 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 60/232,401
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 ; PRIOR APPLICATION NUMBER: 60/241,808
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 ; PRIOR APPLICATION NUMBER: 60/241,826
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 ; PRIOR APPLICATION NUMBER: 60/241,786
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 ; PRIOR APPLICATION NUMBER: 60/241,221
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,475
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/231,243
 ; PRIOR FILING DATE: 2000-09-08

Query Match 54.3%; Score 50; DB 15; Length 272;
 Best Local Similarity 53.8%; Pred. No. 5.5;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CVCCKEPMTSAC 16
 Db 172 CFTCEPTPTGTC 184

RESULT 5
 US-10-114-153-90
 ; Sequence 90, Application US/10114153
 ; Publication No. US20030185815A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Mezes, Peter
 ; APPLICANT: Smithson, Glennnda
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: zerhusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangolli, Esha

; APPLICANT: Vernet, Corine
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Heyes, Melvyn
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Peyman, John
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC AC
 ; FILE REFERENCE: 21402-322A
 ; CURRENT APPLICATION NUMBER: US/10/114,153
 ; CURRENT FILING DATE: 2002-08-06
 ; PRIOR APPLICATION NUMBER: 60/281086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283444
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284234
 ; PRIOR FILING DATE: 2001-04-17
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 251
 ; SEQ ID NO 90
 ; LENGTH: 612
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-114-153-90

Query Match 54.3%; Score 50; DB 12; Length 612;
 Best Local Similarity 53.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CVCCKEPMTSAC 16
 Db 547 CFTCEPTPTGTC 559

RESULT 6
 US-09-764-864-1433
 ; Sequence 1433, Application US/09764864
 ; Patent No. US20020132753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PT223
 ; CURRENT APPLICATION NUMBER: US/09/764,864
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1792
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1433
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-764-864-1433

Query Match 52.2%; Score 48; DB 10; Length 270;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSA 14
 | | | | |
 Db 199 CTTCKQPFTSA 209

RESULT 7

US-09-925-301-1119
 ; Sequence 1119, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PAL06
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1119
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (170)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-301-1119

Query Match 52.2%; Score 48; DB 9; Length 293;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSA 14
 | | | | |
 Db 199 CTTCKQPFTSA 209

RESULT 8

US-09-978-295A-454
 ; Sequence 454, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2630P1C11
 CURRENT APPLICATION NUMBER: US/09/978,295A
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
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 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 50.0%; Score 46; DB 10; Length 125;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 2 LKCYTCKEP-----MTSAC 16
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Db 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 9

US-09-978-697-454
; Sequence 454, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

[illegible]

; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 50.0%; Score 46; DB 10; Length 125;

Best Local Similarity 42.9%; Pred. No. 10;

Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 2 LKCYCKEP-----MTSAC 16
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 DB 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 10

US-09-978-192A-454
 ; Sequence 454, Application US/09978192A
 ; Patent No. US20020177553A1

; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
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 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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18 Best Local Similarity 42.9%; Pred
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28 ; Publication No. US20020192706A1
29 ; GENERAL INFORMATION:
30 ; APPLICANT: Ashkenazi, Avi
31 ; APPLICANT: Baker Kevin P.
32 ; APPLICANT: Botstein, David
33 ; APPLICANT: Desnovers, Luc
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56 ; APPLICANT: Wood, William I.
57 ; TITLE OF INVENTION: Secreted and Tr
58 ; TITLE OF INVENTION: Acids Encoding
59 ; FILE REFERENCE: P2630PIC63
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Query Match 50.0%; Score 46; DB 10; Length 125;

Best Local Similarity 42.9%; Pred. No. 10; Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

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Db 23 LRCVCEPTGVSDCVTIATC 43

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RESULT 12

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; US-09-978-189-454
; Sequence 454, Application US/09978189
; Publication No. US20030004102A1

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GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match          50.0%; Score 4
Best Local Similarity 42.9%; Pred. N
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DB 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 13
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; APPLICANT: Ashkenazi, Avi
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; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
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; TITLE OF INVENTION: Secreted and Transferred
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; CURRENT APPLICATION NUMBER: US/09/978-608A
; CURRENT FILING DATE: 2001-10-16
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; ORGANISM: Homo sapiens
US-09-978-608A-454

Query Match          50.0%; Score 4
Best Local Similarity 42.9%; Pred. N
Matches              9; Conservative 2; Mismatches 4

QY 2 LKCYTCKEP-----MTSAAC 16
DB 23 LRCYVCPEPTGVSDCVTIATC 43

RESULT 14
US-09-978-585A-454
; Sequence 454, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

```



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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Steward, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C5
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 454
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-454

Query Match      50.0%; Score 46; DB 11; Length 125;
Best Local Similarity 42.9%; Pred. NO. 10;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy      2 LKCVTKCEP-----MTSAAC 16
      |||||
Db      23 LRCVVCPEPTGSCVVIATC 43

RESULT 15
US-09-978-191A-454
; Sequence 454, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Steward, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C5
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 454
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-454

; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
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; PRIOR APPLICATION NUMBER: 60/081049
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; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/081817
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; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR APPLICATION NUMBER: 60/081952
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; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 50.0%; Score 46; DB 11; Length 125;
 Best Local Similarity 42.9%; Pred. No. 10;
 Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

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Qy      2 LKCYTCKP-----MTSAC 16
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Db      23 LRCYVCPEPTGVSDCVTIATC 43

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Search completed: October 9, 2003, 14:13:48
 Job time : 27 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 14:08:17 ; Search time 29 Seconds
(without alignments)
23.344 Million cell updates/sec

Title: US-08-986-606E-1
Perfect score: 92
Sequence: 1 ELKCYTCKEPMWTSAAAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84	91.3	81	2	US-08-448-561-1
2	84	91.3	103	2	US-08-448-561-4
3	42	45.7	272	4	US-09-199-637A-285
4	42	45.7	272	4	US-09-252-991A-21429
5	41	44.6	355	4	US-09-352-991A-21002
6	41	44.6	409	4	US-09-724-864-53
7	41	44.6	1404	4	US-08-801-308-1
8	40	43.5	61	2	US-08-785-530-6
9	40	43.5	61	2	US-09-123-850-6
10	40	43.5	123	3	US-08-675-508-2
11	40	43.5	123	3	US-09-203-939-2
12	40	43.5	123	3	US-09-203-939-4
13	40	43.5	123	3	US-09-203-939-6
14	40	43.5	123	3	US-09-203-939-7
15	40	43.5	123	3	US-09-251-835-2
16	40	43.5	123	3	US-09-251-835-4
17	40	43.5	123	3	US-09-251-835-6
18	40	43.5	123	3	US-09-251-835-7
19	40	43.5	123	3	US-09-318-503-2
20	40	43.5	123	3	US-09-318-503-4
21	40	43.5	123	3	US-09-318-503-6
22	40	43.5	123	3	US-09-318-503-7
23	40	43.5	123	3	US-09-038-261A-2
24	40	43.5	123	3	US-09-038-261A-4
25	40	43.5	123	3	US-09-038-261A-6
26	40	43.5	123	3	US-09-038-261A-7
27	40	43.5	123	4	US-09-564-329A-2

28	40	43.5	123	4	US-09-564-329A-4	Sequence 4, Appli
29	40	43.5	123	4	US-09-564-329A-6	Sequence 6, Appli
30	40	43.5	123	4	US-09-564-329A-7	Sequence 7, Appli
31	40	43.5	375	2	US-07-857-224B-86	Sequence 86, Appli
32	40	43.5	1317	3	US-09-083-521-7	Sequence 7, Appli
33	40	43.5	1384	3	US-08-976-255-11	Sequence 11, Appli
34	40	43.5	2291	2	US-08-286-819A-29	Sequence 29, Appli
35	40	43.5	2291	3	US-08-980-357-29	Sequence 29, Appli
36	38.5	41.8	187	3	US-08-545-860D-59	Sequence 59, Appli
37	38.5	41.8	187	5	PCT-US94-04496-59	Sequence 59, Appli
38	38.5	41.8	330	1	US-08-468-853-6	Sequence 6, Appli
39	38.5	41.8	330	1	US-08-468-855-6	Sequence 6, Appli
40	38.5	41.8	330	1	US-08-310-357-6	Sequence 6, Appli
41	38.5	41.8	330	1	US-08-468-852-6	Sequence 6, Appli
42	38.5	41.8	330	2	US-08-468-857-6	Sequence 6, Appli
43	38	41.3	25	2	US-08-620-151-132	Sequence 132, App
44	38	41.3	99	4	US-09-252-991A-31913	Sequence 31913, A
45	38	41.3	106	3	US-09-383-586-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-08-448-561-1
; Sequence 1, Application US/08448561
; Patent No. 5908827
; GENERAL INFORMATION:
; APPLICANT: SIRNA, Antonio
; TITLE OF INVENTION: NEW PROTEIN FROM URINE NAMED COMPONENT B
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,561
; FILING DATE: 22-JAN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT RM 92 A/919
; FILING DATE: 22-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SIRNA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: URINE
; US-08-448-561-1

Query Match 91.3%; Score 84; DB 2; Length 81;
Best Local Similarity 93.3%; Pred. No. 3.9e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-252-991A-21002
; Sequence 21002, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21002
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21002

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Query Match 44.6%; Score 41; DB 4; Length 355;
 Best Local Similarity 46.2%; Pred. No. 72;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 CYTCKEPMTSAAC 16
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 Db 329 CWSCTPPHRSASC 341

RESULT 6
 US-09-724-864-53
 ; Sequence 53, Application US/09724864
 ; Patent No. 6380362
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Murison, James G.
 ; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
 ; TITLE OF INVENTION: by the polynucleotides and methods for their use.
 ; FILE REFERENCE: 11000.105001
 ; CURRENT APPLICATION NUMBER: US/09/724,864
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/171,678
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 53
 ; LENGTH: 409
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-724-864-53

Query Match 44.6%; Score 41; DB 4; Length 409;
 Best Local Similarity 57.1%; Pred. No. 83;
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Qy 3 KYCTCKEPMTSAAAC 16
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 Db 200 KYYCRE--TEPAC 211

RESULT 7
 US-08-801-308-1
 ; Sequence 1, Application US/08801308
 ; Patent No. 6368790
 ; GENERAL INFORMATION:
 ; APPLICANT: Scott, Robert E.
 ; TITLE OF INVENTION: CDNA ENCODING P2P PROTEINS AND USE OF
 ; TITLE OF INVENTION: P2P CDNA-DERIVED ANTIBODIES AND ANTISENSE REAGENTS IN
 ; TITLE OF INVENTION: DETERMINING THE PROLIFERATIVE POTENTIAL OF NORMAL,
 ; TITLE OF INVENTION: ABNORMAL AND CANCER CELLS IN ANIMALS AND HUMANS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Weiser & Associates, P.C.
 ; STREET: 230 S. Fifteenth Street, Suite 500
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/801,308
 ; FILING DATE: 18-FEB-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weiser, Gerard J.
 ; REGISTRATION NUMBER: 19,763
 ; REFERENCE/DOCKET NUMBER: 372.6435P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-801-308-1

Query Match 44.6%; Score 41; DB 4; Length 1404;
 Best Local Similarity 57.1%; Pred. No. 2.9e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ELKCYTCKEPMTSA 14
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 Db 58 ELLCLICKDIMTDA 71

RESULT 8
 US-08-785-530-6
 ; Sequence 6, Application US/08785530
 ; Patent No. 5814480
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Goli, Surya K.
 ; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONEIN
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/785,530
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0194 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:

INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 61 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 305363
 ; US-08-785-530-6

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 Matches 9; Conservative 2; Mismatches 5; Indels 6; Gaps 1;
 Qy 1 ELKCYTCKE-----PMTSAAC 16
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 Db 23 ECKCTTCKKSCSCCPVCAKC 44

RESULT 9
US-09-123-850-6
; Sequence 6, Application US/09123850
; Patent No. 5955428
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: A NOVEL HUMAN METALLOTHIONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09123,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0194 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 305363
US-09-123-850-6
Query Match 43.5%; Score 40; DB 2; Length 61;
Best Local Similarity 40.9%; Pred. No. 17;
Matches 9; Conservative 2; Mismatches 5; Indels 5; Gaps 1;
Qy 1 ELKCYTKCE-----PMTSAAC 16
Db 23 ECKCTTKKSCSCCPVCAK 44
RESULT 10
US-08-675-508-2
; Sequence 2, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: SCAH-2
CLONE:
US-08-675-508-2
Query Match 43.5%; Score 40; DB 2; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 5; Gaps 0;
Qy 2 LKCYTCKEPMTSAAC 16
Db 21 LLCYSCKAQVSNEDC 35
RESULT 11
US-09-203-939-2
; Sequence 2, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-203-939-2
Query Match 43.5%; Score 40; DB 3; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16
 | | | | | : : : |
 Db 21 LLCYSCKAQVSNEDC 35

RESULT 12
 US-09-203-939-4
 ; Sequence 4, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: MURINE PSCA (mpSCA)
 US-09-203-939-4

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16
 | | | | | : : : |
 Db 21 LQCYCTAQMNDRD 35

RESULT 13
 US-09-203-939-6
 ; Sequence 6, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: HUMAN PSCA (hpSCA)
 US-09-203-939-6

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16

Db 21 LLCYSCKAQVSNEDC 35
 | | | | | : : : |

RESULT 14
 US-09-203-939-7
 ; Sequence 7, Application US/09203939
 ; Patent No. 6258939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US11
 ; CURRENT APPLICATION NUMBER: US/09/203,939
 ; CURRENT FILING DATE: 2000-12-02
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: MURINE PSCA (mpSCA)
 US-09-203-939-7

Query Match 43.5%; Score 40; DB 3; Length 123;
 Best Local Similarity 40.0%; Pred. No. 34;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAAC 16
 | | | | | : : : |
 Db 21 LQCYCTAQMNDRD 35

RESULT 15
 US-09-251-835-2
 ; Sequence 2, Application US/09251835A
 ; Patent No. 6261789
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
 ; FILE REFERENCE: 30435.54US12
 ; CURRENT APPLICATION NUMBER: US/09/251,835A
 ; CURRENT FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: HUMAN PSCA (hpSCA)
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (50)...(64)
 ; NAME/KEY: SITE
 ; LOCATION: (71)...(82)
 ; NAME/KEY: SITE

; LOCATION: (67) .. (81)
US-09-251-835-2

Query Match 43.5%; Score 40; DB 3; Length 123;
Best Local Similarity 40.0%; Pred. No. 34;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 LKCYTCKEPMTSAC 16
Db 21 LLCYSCKAQVSNEDC 35

Search completed: October 9, 2003, 14:13:14
Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 14:03:46 ; Search time 83 Seconds
(without alignments)
30.598 Million cell updates/sec

Title: US-08-986-606E-1

Perfect score: 92

Sequence: 1 ELKCYTCKEPTMSAAC 16

Scoring table:

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	23	N-terminal peptide
2	84	91.3	81	20	Human LUS-1 protei
3	84	91.3	103	15	Component B protei
4	84	91.3	103	21	Human PRO2038 prot
5	79	85.9	15	21	Antineoplastic uri
6	78	84.8	14	15	Antineoplastic uri
7	75	81.5	14	15	Antineoplastic uri
8	58	63.0	558	22	Peptide #5203 enco
9	58	63.0	739	22	Novel human diagno

10	52	56.5	2931	22	ABE68229	Drosophila melanog
11	50	54.3	212	22	AAW99933	Human polypeptide
12	50	54.3	272	22	AAW99920	Human polypeptide
13	50	54.3	514	24	ABU11798	Human MDDT polypep
14	50	54.3	612	24	ABU12085	Human NOV26a CG938
15	48	52.2	240	23	AGG66137	Human MPO-110 poly
16	48	52.2	270	22	AAU16480	Human novel secret
17	48	52.2	270	24	ABU55549	Human novel polype
18	48	52.2	293	21	AAW43674	Human cancer assoc
19	48	52.2	773	23	AGG66135	Human MPO-110 poly
20	48	52.2	773	23	AGG66136	Human MPO-110 poly
21	48	52.2	835	24	ABU56447	Lung cancer-associ
22	47	51.1	55	22	AAW49256	Ap LIM domain 1.
23	47	51.1	132	23	AAU09169	Human heat shock p
24	47	51.1	320	22	AAU04898	Micromonospora eve
25	46	50.0	84	22	AAE03360	Human gene 10 enco
26	46	50.0	125	20	AAV41756	Human PRO788 prote
27	46	50.0	125	21	AAW44312	Human PRO788 (ONQ4
28	46	50.0	125	21	AAW33439	Human PRO788 prote
29	46	50.0	125	21	AAW24415	Human growth facto
30	46	50.0	125	21	AAW03000	Human gene 10 enco
31	46	50.0	125	22	AAE03301	Human gene 10 enco
32	46	50.0	125	22	AAE03327	Human gene 10 enco
33	46	50.0	125	22	AAW50915	Human PRO788 prote
34	46	50.0	125	23	ABG64428	Human albumin fusi
35	46	50.0	125	23	ABG64430	Human albumin fusi
36	46	50.0	125	23	ABW95477	Human angioogenesis
37	46	50.0	125	23	ABB84871	Human PRO788 prote
38	46	50.0	125	23	AAU83661	Human PRO788 prote
39	46	50.0	125	24	ABU61142	Human PRO788 polyp
40	44	47.8	79	20	AAV27322	Rat CDS9 protein f
41	44	47.8	136	23	AAE14727	Human Alzheimer's
42	44	47.8	214	19	AAW98557	H. pylori GHPO 168
43	43	46.7	148	22	ABW67787	Drosophila melanog
44	43	46.7	155	22	ABW9452	Human papillomavir
45	43	46.7	469	22	ABW58444	Drosophila melanog

ALIGNMENTS

RESULT 1

ABW83280

1. ABW83280 standard; peptide; 16 AA.

XX

AC

ABW83280;

XX

DT 29-AUG-2002 (first entry)

XX

DE N-terminal peptide fragment of Antineoplastic protein, ANUP.

XX

KW Antineoplastic protein; ANUP; cytostatic; antitumour; apoptosis; tumour.

XX

OS Synthetic.

XX

FH Key

FT Modified-site 1

FT /note= "Pyroglutamic acid"

XX

PN US2002061851-A1.

XX

PD 23-MAY-2002.

XX

PF 08-DEC-1997; 97US-0986606.

XX

PR 08-DEC-1997; 97US-0986606.

XX

PA (SLAO/) SLAONE N H.

XX

PI Slaone NH;

XX

DR WPI; 2002-489588/52.

XX

PT Use of partial N-terminal hexadeca peptide of antineoplastic protein to
 PT kill human tumor cells using human breast tumor cell line as model -
 XX
 PS Claim 2; Page 2; 3pp; English.
 XX
 CC The present sequence is an N-terminal peptide fragment of the
 CC Antineoplastic protein (ANUP). This peptide is a pharmacologically active
 CC antitumour agent, and has approx. 50% of the ANUP protein's anti-tumour
 CC activity with only 10% of the molecular weight. This peptide is claimed
 CC to exert its action by killing tumour cells (apoptosis). Antitumour
 CC activity is only achieved in the presence of sodium dodecyl sulphate
 CC (SDS).
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 100.0%; Score 92; DB 23; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELKCYTCKEPTMSAAC 16
 DB 1 ELKCYTCKEPTMSAAC 16
 RESULT 2
 AAW94613
 ID AAW94613 standard; protein; 81 AA.
 XX
 AC AAW94613;
 XX
 XX 28-APR-1999 (first entry)
 DT
 DE Human LUS-I protein.
 XX
 XX Human; LUS-I; infection; cancer; autoimmune disease; oedema; asthma;
 KW paroxysmal nocturnal haemoglobinuria; diagnosis.
 KW
 OS Homo sapiens.
 XX
 XX WO9856810-A2.
 PN
 XX 17-DEC-1998.
 PD
 XX 09-JUN-1998; 98WO-EP03460.
 PF
 XX 06-NOV-1997; 97DE-1049073.
 PR
 XX 09-JUN-1997; 97DE-1024301.
 XX
 XX (FORS/) FORSMANN W.
 PA
 XX Adermann K, Bensch K, Forssmann W, Heine G, Meyer M;
 PI Nehls M, Schulz-Knappe P;
 PI
 XX WPI; 1999-080884/07.
 XX
 XX New protein, LUS-I, and related nucleic acid, antibodies, inhibitors
 PT and transgenic animals - for treatment and diagnosis of infections,
 PT cancer, autoimmune disease, oedema, asthma and paroxysmal nocturnal
 PT haemoglobinuria
 XX
 XX Claim 1; Page 9; 12pp; German.
 PS
 CC The present sequence represents a human protein designated LUS-I.
 CC The present invention also describes its cyclic, glycosylated,
 CC phosphorylated, acetylated, amidated or side chain-coupled derivatives
 CC and biologically active fragments. The LUS-I protein, nucleotide
 CC sequence and antibodies can be used for diagnosis and treatment of
 CC bacterial and viral infections; under- or over-expression of LUS-I;
 CC cancer (of the cervix uteri; small cell bronchial, pancreatic or mammary
 CC carcinomas, or melanoma); autoimmune diseases; angioneurotic oedema;
 CC bronchial asthma or paroxysmal nocturnal haemoglobinuria. LUS-I
 CC nucleotide sequences are also useful for treating (non-)somatic genetic
 CC disorders associated with inadequate or abnormal expression of LUS-I.

CC Transgenic animals are useful for studying effects of LUS-I on formation
 CC and development of tumours. Diagnostically, antibodies are used in
 CC standard immunoassays to detect the protein in tissues and body fluids,
 CC while analysis of the nucleotide sequence (particularly by amplification)
 CC is used to detect diseases that can be treated with the protein.
 XX
 XX Sequence 81 AA;
 SQ
 Query Match 91.3%; Score 84; DB 20; Length 81;
 Best Local Similarity 93.3%; Pred. No. 2.5e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LKCYTCKEPTMSAAC 16
 DB 1 LKCYTCKEPTMSAAC 15
 RESULT 3
 AAR70984
 ID AAR70984 standard; Protein; 103 AA.
 XX
 AC AAR70984;
 XX
 XX 25-MAR-2003 (updated)
 DT 27-JUL-1995 (first entry)
 DT
 XX Component B protein.
 DE
 XX Probe; component B; promoter; human; signal peptide; primer; RACE;
 KW low molecular weight protein; urine; TGF-alpha; receptor; amplify;
 KW inflammation; coagulation; tumour; angiogenesis.
 XX
 XX Homo sapiens.
 OS
 XX WO9414959-A1.
 PN
 XX 07-JUL-1994.
 PD
 XX 21-DEC-1993; 93WO-EP03645.
 PF
 XX 22-DEC-1992; 92IT-RM00919.
 PR
 XX (ISTF) ARS APPLIED RES SYST HOLDING NV.
 PA
 XX Sirna A;
 PI
 XX WPI; 1994-234696/28.
 DR
 XX N-PSDB; AAQ87876, AAQ87878.
 XX
 XX New protein, component B, isolated from urine - with
 PT antiinflammatory, anticoagulant and anti-tumour activities, also
 PT related nucleic acid, vectors and transformed cells.
 PT
 XX Claim 1; Fig 2; 55pp; English.
 PS
 XX This sequence represents the genomic sequence encoding component B.
 CC This sequence was isolated using the probes given in AAQ87854-69.
 CC The component B gene contains three exons and two introns.
 CC Exon 1 is 84 bp and contains 26 bases of untranslated mRNA. It
 CC encodes 19 amino acids of the putative signal peptide and is
 CC separated from exon 2 by an intron of 410 bp. Exon 2 is 120 bp and
 CC codes for 3 amino acids of the putative signal sequence and 37 amino
 CC acids of the mature protein. It is separated from exon 3 by an
 CC intron of about 550 bp. Exon 3 is 326 bp and encodes the C-terminal
 CC 44 amino acids of component B, and 192 bases of untranslated RNA which
 CC contains a poly-A signal 14 bp upstream of the 3' processing site.
 CC Component B is a low molecular weight protein which may be isolated
 CC from human urine by adsorption at acid pH on kaolin, then extraction
 CC with sodium hydroxide. It inhibits binding of TGF-alpha to its
 CC receptor, and so has antiinflammatory, anticoagulant and/or antitumour
 CC activities. It may also be used to treat conditions associated with
 CC altered levels of TGF-alpha, eg. behavioural or hormonal disturbances and
 CC angiogenesis.

CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 103 AA;

Query Match 91.3%; Score 84; DB 15; Length 103;
 Best Local Similarity 93.3%; Pred. No. 3.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKCYTCKEPMPTSAAC 16
 |||||
 Db 23 LKCYTCKEPMPTSAAC 37

RESULT 4
 AAB24039
 ID AAB24039 standard; Protein; 103 AA.
 XX
 AC AAB24039;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Human PRO2038 protein sequence SEQ ID NO:53.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumourigenesis; anticancer; detection.
 XX
 OS Homo sapiens.
 XX
 XX WO2000053750-A1.
 PN
 XX
 PD 14-SEP-2000.
 XX
 XX 02-DEC-1999; 99WO-US28551.
 PF
 XX 08-MAR-1999; 99WO-US05028.
 PR
 PR 01-SEP-1999; 99WO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28634.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 PI
 XX WPI; 2000-594320/56.
 DR
 DR N-PSDB; AAC58121.
 XX
 XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals; and to identify inhibitors of PRO
 PT polypeptide activity or expression -
 XX
 XX Claim 61; Fig 38; 226pp; English.

XX The present invention describes an antibody that binds to a human
 CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780;
 CC PRO4344; PRO1297; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354;
 CC PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has
 CC anticancer activity and can be used to diagnose tumours in mammals, by
 CC detecting complex formation when the antibody is contacted with test
 CC cells. Increased expression of genes encoding (I) can also be detected
 CC to diagnose tumours. Agents which inhibit the activity of (I),
 CC especially the antibodies, or an antisense oligonucleotide which
 CC hybridises to genes encoding (I), can be used to inhibit tumour growth,
 CC preferably by inducing cell death. Methods from the present invention
 CC can be used to identify compounds which inhibit the biological activity
 CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation
 CC probes used in examples from the present invention for human PRO
 CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.

XX Sequence 103 AA;
 SQ

Query Match 91.3%; Score 84; DB 21; Length 103;
 Best Local Similarity 93.3%; Pred. No. 3.2e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKCYTCKEPMPTSAAC 16
 |||||
 Db 23 LKCYTCKEPMPTSAAC 37

RESULT 5
 AAW03300
 ID AAW03300 standard; peptide; 15 AA.
 XX
 AC AAW03300;
 XX
 DT 22-DEC-1997 (first entry)
 XX
 DE Antineoplastic urinary protein blocked N-terminal sequence.
 XX
 KW ANUP; antineoplastic urinary protein; cytokine; anticancer.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "pyroglutamyl residue"
 FT Misc-difference 13
 FT /label= Ser, Thr
 FT /note= "It is uncertain which of Ser and Thr is
 FT present in this position"
 XX
 XX US5298604-A.
 PN
 XX 29-MAR-1994.
 PD
 XX 02-SEP-1993; 93US-0116539.
 PF
 XX 27-JUL-1992; 92US-0919885.
 PR
 PR 02-SEP-1993; 93US-0116539.
 PR
 XX (SLOA/) SLOANE N H.
 DA
 XX
 XX Sloane NH;
 PI
 XX WPI; 1994-100399/12.
 DR
 XX Partial free N-terminal sequence of antineoplastic urinary protein -
 PT useful for cancer therapy
 PT
 XX Disclosure; -; 4pp; English.

XX The invention relates to the elucidation of the partial N-terminal
 CC amino acid sequence of antineoplastic urinary protein (ANUP). This
 CC antitumour cytokine is present in human granulocytes and is excreted
 CC from the serum into the urine. The protein contains a blocked N-terminal
 CC amino acid, the blocking group of which has been identified as a
 CC pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer
 CC 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free
 CC N-terminal amino group. The deblocked protein is transblotted and the
 CC amino acid sequence of the electrophoretically homogeneous deblocked
 CC protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-
 CC Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential
 CC antitumour chemotherapeutic agent to treat human neoplastic disease, as
 CC it is non-toxic to human cells, specifically inhibits only human cancer
 CC cell lines and causes regression of human tumour cell lines implanted in
 CC nude mice.
 CC The present sequence represents the pyroglutamyl-blocked N-terminal
 CC sequence of ANUP, as deduced from its description in the patent.

XX Sequence 15 AA;
 SQ

Query Match 85.9%; Score 79; DB 15; Length 15;
 SQ

Best Local Similarity 93.3%; Pred. No. 2.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELKCYTCCKEPMTSAA 15
|||||||

Db 1 ELKCYTCCKEPMTXAA 15
|||||||

RESULT 6

AAW03299
ID AAW03299 standard; peptide; 14 AA.

XX
AC AAW03299;

XX 22-DEC-1997 (first entry)

XX Antineoplastic urinary protein deblocked N-terminal sequence.

XX ANUP; antineoplastic urinary protein; cytokine; anticancer.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 12
FT /note= "it is unsure whether this residue is Ser or
Thr (see also AAW03298 and AAW03300)"

XX US5298604-A.

XX 29-MAR-1994.

XX 02-SEP-1993; 93US-0116539.

XX 27-JUL-1992; 92US-0919885.

XX 02-SEP-1993; 93US-0116539.

XX (SLOA/) SLOANE N H.

XX Sloane NH;

XX WPI; 1994-100399/12.

XX Partial free N-terminal sequence of antineoplastic urinary protein -
useful for cancer therapy

XX Claim 2; Column 6; 4pp; English.

XX The invention relates to the elucidation of the partial N-terminal
XX amino acid sequence of antineoplastic urinary protein (ANUP). This
XX antitumour cytokine is present in human granulocytes and is excreted
XX from the serum into the urine. The protein contains a blocked N-terminal
XX amino acid, the blocking group of which has been identified as a
XX pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer
XX 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free
XX N-terminal amino group. The deblocked protein is transblotted and the
XX amino acid sequence of the electrophoretically homogeneous deblocked
XX protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-
XX Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential
XX antitumour chemotherapeutic agent to treat human neoplastic disease, as
XX it is non-toxic to human cells, specifically inhibits only human cancer
XX cell lines and causes regression of human tumour cell lines implanted in
XX nude mice.

XX The present sequence represents one of the two possibilities of the
XX deblocked N-terminal sequence as given above.

XX Sequence 14 AA;

Query Match 84.8%; Score 78; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPMTSAA 15
|||||||

Db

RESULT 8
ABB37697

Db 1 LKCYTCCKEPMTSAA 14
RESULT 7
AAW03298
ID AAW03298 standard; peptide; 14 AA.
XX
XX AAW03298;

XX 22-DEC-1997 (first entry)

XX Antineoplastic urinary protein deblocked N-terminal sequence.

XX ANUP; antineoplastic urinary protein; cytokine; anticancer.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 12
FT /note= "it is unsure whether this residue is Thr or
Ser (see also AAW03299 and AAW03300)"

XX US5298604-A.

XX 29-MAR-1994.

XX 02-SEP-1993; 93US-0116539.

XX 27-JUL-1992; 92US-0919885.

XX 02-SEP-1993; 93US-0116539.

XX (SLOA/) SLOANE N H.

XX Sloane NH;

XX WPI; 1994-100399/12.

XX Partial free N-terminal sequence of antineoplastic urinary protein -
useful for cancer therapy

XX Claim 1; Column 6; 4pp; English.

XX The invention relates to the elucidation of the partial N-terminal
XX amino acid sequence of antineoplastic urinary protein (ANUP). This
XX antitumour cytokine is present in human granulocytes and is excreted
XX from the serum into the urine. The protein contains a blocked N-terminal
XX amino acid, the blocking group of which has been identified as a
XX pyroglutamyl residue. The electrophoretically homogeneous ANUP (monomer
XX 16 kD) is treated with pyroglutamyl aminopeptidase to liberate the free
XX N-terminal amino group. The deblocked protein is transblotted and the
XX amino acid sequence of the electrophoretically homogeneous deblocked
XX protein is determined. It is found to be Leu-Lys-Cys-Tyr-Thr-Cys-Lys-
XX Glu-Pro-Met-Thr-(Thr or Ser)-Ala-Ala. ANUP may be utilised as a potential
XX antitumour chemotherapeutic agent to treat human neoplastic disease, as
XX it is non-toxic to human cells, specifically inhibits only human cancer
XX cell lines and causes regression of human tumour cell lines implanted in
XX nude mice.

XX The present sequence represents one of the two possibilities of the
XX deblocked N-terminal sequence as given above.

XX Sequence 14 AA;

Query Match 81.5%; Score 75; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 9.7e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKCYTCCKEPMTSAA 15
|||||||

Db 1 LKCYTCCKEPMTTAA 14
|||||||

ID ABB37697 standard; Peptide; 558 AA.
AC ABB37697;
XX
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #5203 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
XX WO200157277-A2.
PN
PD
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483447/52.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human fetal liver -
XX
XX Claim 27; SEQ ID NO 30332; 639pp + sequence listing; English.
PS
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a peptide encoded by a single exon
CC nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 558 AA;
Query Match 63.0%; Score 58; DB 22; Length 558;
Best Local Similarity 64.3%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 KCYTCKEPMTSAAC 16
||| | : | : | : |
Db 285 KCYCKGKPTSSAC 298
RESULT 9
ABG03917
ID ABG03917 standard; Protein; 739 AA.
XX
AC ABG03917;
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #3908.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX

PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR N-PSDB; AAS68104.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 34276; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 739 AA;
Query Match 63.0%; Score 58; DB 22; Length 739;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 KCYTCKEPMTSAAC 16
||| | : | : | : |
Db 392 KCYCKGKPTSSAC 405
RESULT 10
ABB68229
ID ABB68229 standard; Protein; 2931 AA.
XX
AC ABB68229;
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 31479.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX

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PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL12332.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 31479; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB116176-AB116175), expressed DNA
XX sequences (AB116176-AB116175) and the encoded proteins
XX (AB116176-AB116175).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2931 AA;
XX
XX
XX Query Match 56.5%; Score 52; DB 22; Length 2931;
XX Best Local Similarity 47.4%; Pred. No. 61;
XX Matches 9; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
XX
XX Qy 2 LKCYCKEPM-...TSAAC 16
XX :|||||:|:|:|
XX 1411 LKCYCKDFCEDPTTSC 1429
XX
XX
XX RESULT 11
XX AAM99933
XX ID AAM99933 standard; Protein; 212 AA.
XX
XX AC AAM99933;
XX
XX DT 07-JAN-2002 (first entry)
XX
XX DE Human polypeptide SEQ ID NO 49.
XX
XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.
XX
XX OS Homo sapiens.
XX
XX PN W0200155173-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01356.
XX
XX PR 31-JAN-2000; 2000US-0179065.
XX
XX PR 04-FEB-2000; 2000US-0180628.
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XX PR 24-FEB-2000; 2000US-0184664.
XX
XX PR 02-MAR-2000; 2000US-0186350.
XX
XX PR 16-MAR-2000; 2000US-0189874.
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XX PR 17-MAR-2000; 2000US-0190076.
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XX
XX 18-APR-2000; 2000US-0198123.
XX
XX 19-MAY-2000; 2000US-0205515.
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XX 07-JUN-2000; 2000US-0209467.
XX
XX 28-JUN-2000; 2000US-0214886.
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XX 30-JUN-2000; 2000US-0215135.
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XX 07-JUL-2000; 2000US-0216647.
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XX 07-JUL-2000; 2000US-0216880.
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XX 11-JUL-2000; 2000US-0217487.
XX
XX 14-JUL-2000; 2000US-0218290.
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XX 26-JUL-2000; 2000US-0220963.
XX
XX 26-JUL-2000; 2000US-0220964.
XX
XX 14-AUG-2000; 2000US-0224518.
XX
XX 14-AUG-2000; 2000US-0224519.
XX
XX 14-AUG-2000; 2000US-0225213.
XX
XX 14-AUG-2000; 2000US-0225214.
XX
XX 14-AUG-2000; 2000US-0225266.
XX
XX 14-AUG-2000; 2000US-0225267.
XX
XX 14-AUG-2000; 2000US-0225268.
XX
XX 14-AUG-2000; 2000US-0225270.
XX
XX 14-AUG-2000; 2000US-0225447.
XX
XX 14-AUG-2000; 2000US-0225757.
XX
XX 14-AUG-2000; 2000US-0225758.
XX
XX 14-AUG-2000; 2000US-0225759.
XX
XX 18-AUG-2000; 2000US-0226279.
XX
XX 22-AUG-2000; 2000US-0226681.
XX
XX 22-AUG-2000; 2000US-0226686.
XX
XX 22-AUG-2000; 2000US-0227182.
XX
XX 22-AUG-2000; 2000US-0227009.
XX
XX 30-AUG-2000; 2000US-0228924.
XX
XX 01-SEP-2000; 2000US-0229287.
XX
XX 01-SEP-2000; 2000US-0229343.
XX
XX 01-SEP-2000; 2000US-0229344.
XX
XX 01-SEP-2000; 2000US-0229345.
XX
XX 05-SEP-2000; 2000US-0229509.
XX
XX 05-SEP-2000; 2000US-0229513.
XX
XX 06-SEP-2000; 2000US-0230437.
XX
XX 06-SEP-2000; 2000US-0230438.
XX
XX 08-SEP-2000; 2000US-0231242.
XX
XX 08-SEP-2000; 2000US-0231243.
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XX 08-SEP-2000; 2000US-0231244.
XX
XX 08-SEP-2000; 2000US-0231413.
XX
XX 08-SEP-2000; 2000US-0231414.
XX
XX 08-SEP-2000; 2000US-0232080.
XX
XX 12-SEP-2000; 2000US-0232081.
XX
XX 14-SEP-2000; 2000US-0231968.
XX
XX 14-SEP-2000; 2000US-0232397.
XX
XX 14-SEP-2000; 2000US-0232398.
XX
XX 14-SEP-2000; 2000US-0232399.
XX
XX 14-SEP-2000; 2000US-0232400.
XX
XX 14-SEP-2000; 2000US-0232401.
XX
XX 14-SEP-2000; 2000US-0233063.
XX
XX 14-SEP-2000; 2000US-0233064.
XX
XX 14-SEP-2000; 2000US-0233065.
XX
XX 21-SEP-2000; 2000US-0234223.
XX
XX 21-SEP-2000; 2000US-0234274.
XX
XX 25-SEP-2000; 2000US-0234997.
XX
XX 25-SEP-2000; 2000US-0234998.
XX
XX 26-SEP-2000; 2000US-0235484.
XX
XX 27-SEP-2000; 2000US-0235834.
XX
XX 27-SEP-2000; 2000US-0235836.
XX
XX 29-SEP-2000; 2000US-0236327.
XX
XX 29-SEP-2000; 2000US-0236367.
XX
XX 29-SEP-2000; 2000US-0236368.
XX
XX 29-SEP-2000; 2000US-0236369.
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XX 29-SEP-2000; 2000US-0236370.
XX
XX 02-OCT-2000; 2000US-0236802.
XX
XX 02-OCT-2000; 2000US-0237037.
XX
XX 02-OCT-2000; 2000US-0237038.
XX
XX 02-OCT-2000; 2000US-0237039.
XX
XX 02-OCT-2000; 2000US-0237040.
XX
XX 13-OCT-2000; 2000US-0239935.
XX
XX 13-OCT-2000; 2000US-0239937.

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PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-451924/48.
XX N-PSDB; AA199531.
XX
XX New nucleic acids and polypeptides, useful for treating, preventing or
XX ameliorating human disorders and diseases -
XX
XX Claim 11; SEQ ID NO 49; 465pp + Sequence Listing; English.
XX
XX The invention relates to novel human polynucleotides (AA199513-AA199538)
XX and the encoded proteins (AAM99915-AAM99934) which are useful for
XX preventing, treating or ameliorating medical conditions e.g. by protein

CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as
CC viral, bacterial, fungal and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 212 AA;

Query Match 54.3%; Score 50; DB 22; Length 212;
Best Local Similarity 53.8%; Pred. No. 8.6;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 CYTCKEPTMTSAAC 16
|:|:|:|:|:
Db 172 CFTCQEPPTSTGC 184

RESULT 12

AAM99920

ID AAM999920 standard; Protein; 272 AA.

XX AAM999920;

DT 07-JAN-2002 (first entry)

XX Human polypeptide SEQ ID NO 36.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulvular; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.

OS Homo sapiens.

XX WO200155173-A2.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01356.

XX

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0217496.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
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PR 29-SEP-2000; 2000US-0236327.
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PR 08-NOV-2000; 2000US-0246611.
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PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451924/48.

N-PSDB; AA199518.

New nucleic acids and polypeptides, useful for treating, preventing or ameliorating human disorders and diseases -

Claim 11; SEQ ID NO 36; 465pp + Sequence Listing; English.

The invention relates to novel human polynucleotides (AA199513-AA199538) and the encoded proteins (AA199513-AA199538) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 272 AA;
 Query Match 54.3%; Score 50; DB 22; Length 272;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSAAC 16
 :||:|:|:|
 Db 172 CFTCQEPPTSTGC 184
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 RESULT 13
 ABU11798
 ID ABU11798 standard; Protein; 514 AA.
 AC ABU11798;
 XX
 DT 13-FEB-2003 (first entry)
 DE Human MDDT polypeptide SEQ ID 745.
 KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US09944.
 XX
 PR 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.
 PR 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;
 PI Daugherty SC, Dam TC, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 DR WPI; 2003-058431/05.
 DR N-PSDS; ABX34788.
 XX
 PT New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis -
 XX
 PS Claim 27; SEQ ID NO 745; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are

CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 514 AA;
 Query Match 54.3%; Score 50; DB 24; Length 514;
 Best Local Similarity 53.8%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 4 CYTCKEPTMTSAAC 16
 :||:|:|:|
 Db 175 CFTCQEPPTSTGC 187
 :||:|:|:|
 RESULT 14
 ABU12085
 ID ABU12085 standard; Protein; 612 AA.
 XX
 AC ABU12085;
 XX
 DT 19-FEB-2003 (first entry)
 DE Human NOV26a CG93871-01 protein SEQ ID 90.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiac;
 KW antilipaeamic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US10366.
 XX
 PR 03-APR-2001; 2001US-281086P.
 PR 05-APR-2001; 2001US-281906P.
 PR 06-APR-2001; 2001US-282020P.
 PR 10-APR-2001; 2001US-282930P.
 PR 12-APR-2001; 2001US-283444P.
 PR 12-APR-2001; 2001US-283512P.
 PR 13-APR-2001; 2001US-283657P.
 PR 13-APR-2001; 2001US-283678P.
 PR 13-APR-2001; 2001US-283710P.
 PR 17-APR-2001; 2001US-284234P.
 PR 19-APR-2001; 2001US-285325P.
 PR 20-APR-2001; 2001US-285381P.
 PR 24-APR-2001; 2001US-286068P.
 PR 25-APR-2001; 2001US-286292P.
 PR 07-JUN-2001; 2001US-296692P.
 PR 26-JUN-2001; 2001US-300883P.
 PR 08-AUG-2001; 2001US-311003P.
 PR 13-AUG-2001; 2001US-311973P.
 PR 16-AUG-2001; 2001US-312901P.
 PR 14-SEP-2001; 2001US-322283P.
 PR 05-OCT-2001; 2001US-327448P.
 PR 31-DEC-2001; 2001US-345734P.
 PR 03-JAN-2002; 2002US-345755P.
 PR 04-FEB-2002; 2002US-354391P.
 PR 02-APR-2002; 2002US-0114153.

XX PA (CURA-) CURAGEN CORP.
XX PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD, Smithson G;
XX PI Guo X, Gerlach V, Caaman SJ, Boldog FL, Li L, Zerhusen BD;
XX PI Thernevi VI, Gangolli EA, Vernet CAM, Spytek KA, Malyankar UM;
XX PI Paturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J, Peyman JA;
XX PI Catterton E, MacDougall JR, Edinger SR, Stone DJ, Mazur A;
XX WPI: 2003-046862/04.
XX N-PSDB: ABX56305.
XX PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
XX PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
XX PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
XX PT cancer -
XX PS Claim 1; Page 188; 425pp; English.
XX CC This invention describes novel polypeptides, termed NOVX which have
XX CC anti-diabetic, anti-arteriosclerotic, anorectic, metabolic, antimicrobial,
XX CC neuroprotective, anti-parkinsonian, antilipemic, cytosstatic, nootropic,
XX CC cardiant and immunomodulatory activity. The polypeptide and any
XX CC antibodies generated from it are useful in the manufacture of a
XX CC medicament for treating a syndrome associated with a human disease
XX CC selected from a pathology associated with the NOVX polypeptide. Fragments
XX CC and portions of the polynucleotides encoding NOVX polypeptides are useful
XX CC to map the location of NOVX genes on a chromosome, to identify
XX CC individuals from minute biological samples, as DNA markers for
XX CC restriction fragment length polymorphism (RFLP), and are useful to
XX CC prepare polymerase chain reaction primers. The products of the invention
XX CC can be used in gene therapy and for treating cardiomyopathy, metabolic
XX CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
XX CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
XX CC disease, immune disorders, haematopoietic disorders, and various
XX CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
XX CC syndrome X and wasting disorders associated with chronic diseases and
XX CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
XX CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306.
XX SQ Sequence 612 AA;
Query Match 54.3%; Score 50; DB 24; Length 612;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 CYTCKEPTMTSAAC 16
|:|:|:|:|:|:|
Db 547 CFTCQEPPTSGC 559
RESULT 15
AAG66137
ID AAG66137 standard; Protein; 240 AA.
XX AC AA:66137;
XX DT 13-MAR-2002 (first entry)
XX DE Human MFQ-110 polypeptide.
XX KW Zinc finger protein; MFQ-110; developmental disorder; neurodegenerative;
XX KW psychiatric; vascular disease; angiogenesis; cancer; human.
XX OS Homo sapiens.
XX PN WO200185765-A2.
XX PD 15-NOV-2001.
XX PF 11-MAY-2001; 2001WO-EP05372.
XX PR 12-MAY-2000; 2000EP-0110089.

(MERE) MERCK PATENT GMBH.
Rodes Gubern B, Messeguer Peypoch R, Masa Alvarez M, Rosell Vives E;
WPI: 2002-055583/07.
N-PSDB: AAI67913.
Identification of a new human C2H2-type finger protein, MFQ-110, which
may be useful in the treatment and diagnosis of disease such as
developmental disorders, neurodegenerative disease, vascular disease
and cancer -
Claim 1; Page 60-61; 63pp; English.
The invention provides new human C2H2-type zinc finger proteins, MFQ-110.
The MFQ-110 polypeptides can be expressed by standard recombinant
methodology. The MFQ-110 polypeptides and polynucleotides can be used in
diagnostic assays for detection of abnormally decreased or increased
levels of polypeptide or mRNA expression. This may be used for diagnosing
or determining susceptibility of a subject to diseases that include
developmental disorders, neurodegenerative disease, brain stroke,
psychiatric disorders such as schizophrenia, cardiac and vascular
disease, angiogenesis and cancer especially lymphomas. The polypeptides
may be used to identify membrane bound or soluble receptors and may be
used to identify agonists and antagonists which compete with receptor
binding. The polynucleotides may be used as diagnostic reagents through
detecting mutations in the associated gene, for chromosome localization
studies and tissue expression studies. The present sequence represents a
human MFQ-110 polypeptide.
XX SQ Sequence 240 AA;
Query Match 52.2%; Score 48; DB 23; Length 240;
Best Local Similarity 72.7%; Pred. No. 20;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 CYTCKEPTMTSA 14
|:|:|:|:|:|:|
Db 172 CTTCCKQPTTSA 182

Search completed: October 9, 2003, 14:09:40
Job time : 84 secs